

GenCore version 5.1.4-p5_4578
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OM nucleic - nucleic search, using sw model

Run on: May 24, 2003, 10:21:51 ; Search time 350.903 Seconds

(Without alignments)
5225.021 Million cell updates/sec

Title: US-09-963-803-11

Perfect score: 63

Sequence: 1 ggcggaagtaacctatgc.....tgcgcgtcccaagcttat 63

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database :

Listing first 45 summaries

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4: gb_cm:.*
5: gb_ov:.*
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7: gb_ph:.*
8: gb_pl:.*
9: gb_pr:.*
10: gb_ro:.*
11: gb_sts:.*
12: gb_sy:.*
13: gb_un:.*
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38: em_sy:.*
39: em_hlg_hum:.*
40: em_hlg_mus:.*
41: em_hlg_other:.*
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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	63	100.0	63	6 AX036745	AX036745 Sequence
2	63	100.0	317	6 AX036737	AX036737 Sequence
3	63	100.0	371	6 AX036739	AX036739 Sequence
4	61.4	97.5	301	6 AX036741	AX036741 Sequence
5	61.4	97.5	348	6 AX036738	AX036738 Sequence
6	61.4	97.5	398	6 AX036740	AX036740 Sequence
7	42	66.7	243	6 AX036735	AX036735 Sequence
8	42	66.7	7489	14 CYWYCG	AX036735 Sequence
9	41.2	65.4	392	6 AX036755	AX036755 Sequence
10	38.8	61.6	604	6 AX036757	AX036757 Sequence
11	37	58.7	472	6 AX036759	AX036759 Sequence
12	37	58.7	541	6 AX036758	AX036758 Sequence
13	35.4	56.2	393	6 AX036753	AX036753 Sequence
14	35.4	56.2	462	6 AX036754	AX036754 Sequence
15	35.4	56.2	600	6 AX036756	AX036756 Sequence
16	35.4	56.2	9285	6 AX036757	AX036757 Sequence
17	35.4	56.2	15077	6 AX036758	AX036758 Sequence
18	27.4	43.5	65142	2 AC121501	AX036759 Sequence
19	27.4	43.5	109395	2 AC13742	AX036759 Sequence
20	27.4	43.5	128821	9 AC108687	AX036759 Sequence
21	27.4	43.5	134236	10 AC024883	AX036759 Sequence
22	27.4	43.5	158987	9 AC108713	AX036759 Sequence
23	27.4	43.5	174327	2 AC068159	AX036759 Sequence
24	26.8	42.5	90111	9 AC008954	AX036759 Sequence
25	26.8	42.5	155013	2 AC026707	AX036759 Sequence
26	26.6	42.2	129564	2 AC087302	AX036759 Sequence
27	26.6	42.2	167932	2 AC068133	AX036759 Sequence
28	26.6	42.2	188800	2 AC015846	AX036759 Sequence
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30	26	41.3	10427	1 AE012158	AX036759 Sequence
31	25.6	40.6	168111	2 AC096061	AX036759 Sequence
32	25.4	40.3	130177	9 HSBG27987	AX036759 Sequence
33	25.4	40.3	131796	9 AC097632	AX036759 Sequence
34	25.4	40.3	186196	2 AC069204	AX036759 Sequence
35	25.2	40.0	189615	2 AC129390	AX036759 Sequence
36	24.8	39.4	539	6 AX062521	AX036759 Sequence
37	24.8	39.4	539	6 AX367438	AX036759 Sequence
38	24.8	39.4	1321	6 A02597	AX036759 Sequence
39	24.8	39.4	4530	1 BACBROXWF	AX036759 Sequence
40	24.8	39.4	89211	9 AL668821	AX036759 Sequence
41	24.8	39.4	129839	9 AL355591	AX036759 Sequence
42	24.8	39.4	161267	9 AC008378	AX036759 Sequence
43	24.8	39.4	201831	2 AC131112	AX036759 Sequence
44	24.6	39.0	95865	8 AC003970	AX036759 Sequence
45	24.6	39.0	146222	2 AC128643	AX036759 Sequence

ALIGNMENTS

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RESULT 1
AX036745
LOCUS AX036745 63 bp DNA
DEFINITION Sequence 11 from Patent WO0058485.
ACCESSION AX036745
VERSION AX036745.1 GI:11226254
KEYWORDS
SOURCE
ORGANISM
SYNTHETIC CONSTRUCT
ARTIFICIAL SEQUENCES
REFERENCE
1 (bases 1 to 63)
Rance, I., Theisen, M. and Gruber, V.
Chimeric expression promoters originating from commelina yellow
mottle virus and cassava vein mosaic virus
Patent: WO 0058485-A II 05-OCT-2000;
JOURNAL
```

MERISTEM THERAPEUTICS (FR) ; RANCE IANN (FR) ; THEISEN MANFRED (FR)
FEATURES
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/db_xref="taxon:32630"
/note="Directional desoxyribo nucleotide building block S4"
BASE COUNT 14 a 14 c 15 g 20 t
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Best Local Similarity 100.0%; Pred. No. 9.7e-15;
Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GGGGGAAGTACCTTATGCTTGTACCTGTTACCCGCTATGCCGTTCCCAAGCTT 60
Db 1 GGGGGAAGTACCTTATGCTTGTACCTGTTACCCGCTATGCCGTTCCCAAGCTT 60
QY 61 TAT 63
Db 61 TAT 63
RESULT 2
AX036737 317 bp DNA linear PAT 16-NOV-2000
LOCUS AX036737
DEFINITION Sequence 3 from Patent WO0058485.
ACCESSION AX036737
VERSION AX036737.1 GI:11226246
KEYWORDS
SOURCE synthetic construct.
ORGANISM synthetic construct.
REFERENCE 1 (bases 1 to 317)
AUTHORS Rance, I., Theisen, M. and Gruber, V.
TITLE Chimeric expression promoters originating from commelina yellow
mottle virus and cassava vein mosaic virus
JOURNAL Patent: WO 0058485-A 3 05-OCT-2000.
MERISTEM THERAPEUTICS (FR) ; RANCE IANN (FR) ; THEISEN MANFRED (FR)
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source
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Location/Qualifiers
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/db_xref="taxon:32630"
/note="promoter MPr1116"
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Best Local Similarity 100.0%; Pred. No. 1.2e-14;
Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 195 GGGGGAAGTACCTTATGCTTGTACCTGTTACCCGCTATGCCGTTCCCAAGCTT 254
QY 61 TAT 63
Db 255 TAT 257
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AX036739 371 bp DNA linear PAT 16-NOV-2000
LOCUS AX036739
DEFINITION Sequence 5 from Patent WO0058485.
ACCESSION AX036739
VERSION AX036739.1 GI:11226248
KEYWORDS
SOURCE synthetic construct.
ORGANISM synthetic construct.
REFERENCE 1 (bases 1 to 371)

AUTHORS Rance, I., Theisen, M. and Gruber, V.
TITLE Chimeric expression promoters originating from commelina yellow
mottle virus and cassava vein mosaic virus
JOURNAL Patent: WO 0058485-A 5 05-OCT-2000.
MERISTEM THERAPEUTICS (FR) ; RANCE IANN (FR) ; THEISEN MANFRED (FR)
FEATURES
source
1. .371
Location/Qualifiers
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/db_xref="taxon:32630"
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Best Local Similarity 100.0%; Pred. No. 1.2e-14;
Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GGGGGAAGTACCTTATGCTTGTACCTGTTACCCGCTATGCCGTTCCCAAGCTT 60
Db 249 GGGGGAAGTACCTTATGCTTGTACCTGTTACCCGCTATGCCGTTCCCAAGCTT 308
QY 61 TAT 63
Db 309 TAT 311
RESULT 4
AX036741 301 bp DNA linear PAT 16-NOV-2000
LOCUS AX036741
DEFINITION Sequence 7 from Patent WO0058485.
ACCESSION AX036741
VERSION AX036741.1 GI:11226250
KEYWORDS
SOURCE synthetic construct.
ORGANISM synthetic construct.
REFERENCE 1 (bases 1 to 301)
AUTHORS Rance, I., Theisen, M. and Gruber, V.
TITLE Chimeric expression promoters originating from commelina yellow
mottle virus and cassava vein mosaic virus
JOURNAL Patent: WO 0058485-A 7 05-OCT-2000.
MERISTEM THERAPEUTICS (FR) ; RANCE IANN (FR) ; THEISEN MANFRED (FR)
FEATURES
source
1. .301
Location/Qualifiers
/organism="synthetic construct"
/db_xref="taxon:32630"
/note="promoter MPr1154"
BASE COUNT 98 a 54 c 74 g 75 t
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Query Match 97.5%; Score 61.4; DB 6; Length 301;
Best Local Similarity 98.4%; Pred. No. 5.4e-14;
Matches 62; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 GGGGGAAGTACCTTATGCTTGTACCTGTTACCCGCTATGCCGTTCCCAAGCTT 60
Db 181 GGGGGAAGTACCTTATGCTTGTACCTGTTACCCGCTATGCCGTTCCCAAGCTT 240
QY 61 TAT 63
Db 241 TAT 243
RESULT 5
AX036738 348 bp DNA linear PAT 16-NOV-2000
LOCUS AX036738
DEFINITION Sequence 4 from Patent WO0058485.
ACCESSION AX036738
VERSION AX036738.1 GI:11226247

KEYWORDS	synthetic construct.
SOURCE	synthetic construct.
ORGANISM	artificial sequences.
REFERENCE	1 (bases 1 to 348)
AUTHORS	Rance,I., Theisen,M. and Gruber,V.
TITLE	Chimeric expression promoters originating from commelina yellow mottle virus and cassava vein mosaic virus
JOURNAL	Patent: WO 0058485-A 4 05-OCT-2000;
	MEISTERM THERAPEUTICS (FR) ; RANCE IANN (FR) ; THEISEN MANFRED (FR)
FEATURES	location/Qualifiers
source	1..348
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	/db_xref="taxon:32630"
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Best Local Similarity	98.4%: Pred. No. 5.5e-14;
Matches 62; Conservative	0; Mismatches 1; Indels 0; Gaps 0;
OY	1 GCGCGAAGTAACCTTATGATTTGTACTTGGTTACCGGATATCCGGTTCCTCAAGCTT 60
Db	228 GCGCGAAGTAACCTTATGATTTGTACTTGGTTACCGGATATCCGGTTCCTCAAGCTT 287
OY	61 TAT 63
Db	288 TAT 290
RESULT 6	
LOCUS	AX036740 398 bp DNA linear PAT 16-NOV-2000
DEFINITION	Sequence 6 from Patent WO0058485.
ACCESSION	AX036740
VERSION	AX036740.1 GI:11226249
KEYWORDS	
SOURCE	synthetic construct.
ORGANISM	artificial construct.
REFERENCE	1 (bases 1 to 398)
AUTHORS	Rance,I., Theisen,M. and Gruber,V.
TITLE	Chimeric expression promoters originating from commelina yellow mottle virus and cassava vein mosaic virus
JOURNAL	Patent: WO 0058485-A 6 05-OCT-2000;
	MEISTERM THERAPEUTICS (FR) ; RANCE IANN (FR) ; THEISEN MANFRED (FR)
FEATURES	location/Qualifiers
source	1..398
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	/db_xref="taxon:32630"
	/note="promoter MP11147"
BASE COUNT	1..398
ORIGIN	128 a 80 c 93 g 97 t
Query Match	97.5%: Score 61.4; DB 6; Length 398;
Best Local Similarity	98.4%: Pred. No. 5.6e-14;
Matches 62; Conservative	0; Mismatches 1; Indels 0; Gaps 0;
OY	1 GCGCGAAGTAACCTTATGATTTGTACTTGGTTACCGGATATCCGGTTCCTCAAGCTT 60
Db	278 GCGCGAAGTAACCTTATGATTTGTACTTGGTTACCGGATATCCGGTTCCTCAAGCTT 337
OY	61 TAT 63
Db	338 TAT 340
RESULT 7	

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            1..7489
                /organism="Commelina yellow mottle virus"
                /db_xref="taxon:10653"
                /clone="pCOYMW89 (and pCOYMW89)"
            1..23
                /product="trna-met"
                /note="put. trna-met (put. primer for minus strand synthesis)"
                /note="302"
                /note="gac was cga"
                /citation=[1]
            496..1098
                /note="orf 1"
                /codon_start=1
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                /db_xref="GI:59048"
                /translation="MNVVLKSHHTPEGLPYSLDPFGFMNOVQVQKRLDMLSSA
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            541
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                /db_xref="GI:59049"
                /translation="MSNTESGKFKALSVTNMYLAPAIGAGADVGLGTVKOLNT
                TLYLAKITQIEDLQSTIKRLERVOSEKATPVYDTPNPETISKLSDIOISLAR
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            1338..1340
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                RSKITSKFDKSGFNOVAEEESVPTALAKNKLYEMLVMPGLNNAITFORKND
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                LGASLCKTKIKLQPHILSKICDFSEKATLPEGMSSMLDLSLYARVYIDIDCKVPL
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Query Match      66.7%: Score 42; DB 14; Length 7489;
Best Local Similarity 100.0%: Pred. No. 6.6e-06;
Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

22 TTGTGTAACGTGTTACCGGTATCGCGTCCAGCTTAT 63
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AX036755      392 bp      DNA      linear      PAT 16-NOV-2000
LOCUS          Sequence 21 from Patent WO0058485.
ACCESSION      AX036755
VERSION        AX036755.1 GI:11226264
KEYWORDS
SOURCE         synthetic construct.
ORGANISM       artificial construct.
REFERENCE      1 (bases 1 to 392)
AUTHORS        Rance, I., Theisen, M. and Gruber, V.
TITLE          ChimERIC expression promoters originating from commelina yellow
               mottle virus and cassava vein mosaic virus
               Patent: WO 0058485-A 21 05-OCT-2000;
               MERISTEM THERAPEUTICS (FR) ; RANCE IANN (FR) ; THEISEN MANFRED (FR)
               ; GRUBER VERONIQUE (FR)
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        Location/Qualifiers
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                /note="promoter MP-1164"
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                Best Local Similarity 79.0%: Pred. No. 9.4e-06;
                Matches 49; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

OY 1 GGGGGAAGTAACCTTATGATTTGTAACCTTATGATGCGGATGCGGTTCCCAAGCTT 60
Db 197 GGGGGAAGTAACCTTATGATTTGTAACCTTATGATGCGGATGCGGTTCCCAAGCTT 296

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Qy 61 TA 62
Db 257 CA 258

RESULT 10
LOCUS AX036757 604 bp DNA Linear PAT 16-NOV-2000
DEFINITION Sequence 23 from Patent WO0058485.
ACCESSION AX036757
VERSION AX036757.1 GI:11226266
KEYWORDS
SOURCE synthetic construct.
ORGANISM synthetic construct.
REFERENCE 1 (bases 1 to 604)
AUTHORS Rance,I., Theisen,M. and Gruber,V.
TITLE ChimERIC expression promoters originating from commelina yellow
mottle virus and cassava vein mosaic virus
JOURNAL Patent: WO 0058485-A 23 05-OCT-2000;
MERISTEM THERAPEUTICS (FR) ; RANCE IANN (FR) ; THEISEN MANFRED (FR)
FEATURES
source location/Qualifiers
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/organism="synthetic construct"
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Promoter 186 a 116 c 145 g 157 t
BASE COUNT
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Best Local Similarity 95.2%; Pred. No. 9.5e-05;
Matches 40; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GCGGAAAGTACCTTATGCACTTGTACTGTTACCCGCT 42
Db 278 GCGGAAAGTACCTTATGCACTTGTACTGTTACTACTACT 319

RESULT 11
LOCUS AX036759 472 bp DNA Linear PAT 16-NOV-2000
DEFINITION Sequence 25 from Patent WO0058485.
ACCESSION AX036759
VERSION AX036759.1 GI:11226268
KEYWORDS
SOURCE synthetic construct.
ORGANISM synthetic construct.
REFERENCE 1 (bases 1 to 472)
AUTHORS Rance,I., Theisen,M. and Gruber,V.
TITLE ChimERIC expression promoters originating from commelina yellow
mottle virus and cassava vein mosaic virus
JOURNAL Patent: WO 0058485-A 25 05-OCT-2000;
MERISTEM THERAPEUTICS (FR) ; RANCE IANN (FR) ; THEISEN MANFRED (FR)
FEATURES
source location/Qualifiers
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/organism="synthetic construct"
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/note="promoter MPr1169"

Promoter 149 a 92 c 112 g 119 t
BASE COUNT
ORIGIN

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Best Local Similarity 100.0%; Pred. No. 0.0005;
Matches 37; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 278 GCGGAAAGTACCTTATGCACTTGTACTGTTAC 314

RESULT 12
LOCUS AX036758 541 bp DNA Linear PAT 16-NOV-2000
DEFINITION Sequence 24 from Patent WO0058485.
ACCESSION AX036758
VERSION AX036758.1 GI:11226267
KEYWORDS
SOURCE synthetic construct.
ORGANISM synthetic construct.
REFERENCE 1 (bases 1 to 541)
AUTHORS Rance,I., Theisen,M. and Gruber,V.
TITLE ChimERIC expression promoters originating from commelina yellow
mottle virus and cassava vein mosaic virus
JOURNAL Patent: WO 0058485-A 24 05-OCT-2000;
MERISTEM THERAPEUTICS (FR) ; RANCE IANN (FR) ; THEISEN MANFRED (FR)
FEATURES
source location/Qualifiers
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/db_xref="taxon:32630"
/note="promoter MPr1168"

Promoter 169 a 104 c 130 g 138 t
BASE COUNT
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Query Match 58.7%; Score 37; DB 6; Length 541;
Best Local Similarity 100.0%; Pred. No. 0.00051;
Matches 37; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 278 GCGGAAAGTACCTTATGCACTTGTACTGTTAC 314

RESULT 13
LOCUS AX036753 393 bp DNA Linear PAT 16-NOV-2000
DEFINITION Sequence 19 from Patent WO0058485.
ACCESSION AX036753
VERSION AX036753.1 GI:11226262
KEYWORDS
SOURCE synthetic construct.
ORGANISM synthetic construct.
REFERENCE 1 (bases 1 to 393)
AUTHORS Rance,I., Theisen,M. and Gruber,V.
TITLE ChimERIC expression promoters originating from commelina yellow
mottle virus and cassava vein mosaic virus
JOURNAL Patent: WO 0058485-A 19 05-OCT-2000;
MERISTEM THERAPEUTICS (FR) ; RANCE IANN (FR) ; THEISEN MANFRED (FR)
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Promoter 128 a 75 c 93 g 97 t
BASE COUNT
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Best Local Similarity 97.3%; Pred. No. 0.0022;
Matches 36; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GCGGAAAGTACCTTATGCACTTGTACTGTTAC 37
Db 197 GCGGAAAGTACCTTATGCACTTGTACTGTTAC 233
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RESULT 14
AX036754      462 bp      DNA      linear      PAT 16-NOV-2000
LOCUS         Sequence 20 from Patent WO0058485.
DEFINITION    AX036754
ACCESSION     AX036754
VERSION       AX036754.1 GI:11226263
KEYWORDS
SOURCE        synthetic construct.
ORGANISM      synthetic construct.
REFERENCE     1 (bases 1 to 462)
AUTHORS      Rance,I., Theisen,M. and Gruber,V.
TITLE        Chimeric expression promoters originating from commelina yellow
              mottle virus and cassava vein mosaic virus
              Patent: WO 0058485-A 20 05-OCT-2000;
              MERISTEM THERAPEUTICS (FR) ; RANCE IANN (FR) ; THEISEN MANFRED (FR)
              ; GRUBER VERONIQUE (FR)
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              /db_xref="taxon:32630"
              /note="promoter MPr1163"
  promoter    1..462
  BASE COUNT  148 a      87 c      111 g      116 t
  ORIGIN
Query Match      56.2%; Score 35.4; DB 6; Length 462;
Best Local Similarity 97.3%; Pred. No. 0.0022;
Matches 36; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 GCGGGAAGTACCTTATGCATTGTGTAACCTGGTTAC 37
        |||||||
Db      197 GCGGGAAGTACCTTATGCATTGTGTAACCTGGTTAC 233

RESULT 15
AX036756      600 bp      DNA      linear      PAT 16-NOV-2000
LOCUS         Sequence 22 from Patent WO0058485.
DEFINITION    AX036756
ACCESSION     AX036756
VERSION       AX036756.1 GI:11226265
KEYWORDS
SOURCE        synthetic construct.
ORGANISM      synthetic construct.
REFERENCE     1 (bases 1 to 600)
AUTHORS      Rance,I., Theisen,M. and Gruber,V.
TITLE        Chimeric expression promoters originating from commelina yellow
              mottle virus and cassava vein mosaic virus
              Patent: WO 0058485-A 22 05-OCT-2000;
              MERISTEM THERAPEUTICS (FR) ; RANCE IANN (FR) ; THEISEN MANFRED (FR)
              ; GRUBER VERONIQUE (FR)
FEATURES
  source      1..600
              location/Qualifiers
              /organism="synthetic construct"
              /db_xref="taxon:32630"
              /note="promoter MPr1165"
  promoter    1..600
  BASE COUNT  188 a      111 c      147 g      154 t
  ORIGIN
Query Match      56.2%; Score 35.4; DB 6; Length 600;
Best Local Similarity 97.3%; Pred. No. 0.0023;
Matches 36; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 GCGGGAAGTACCTTATGCATTGTGTAACCTGGTTAC 37
        |||||||
Db      197 GCGGGAAGTACCTTATGCATTGTGTAACCTGGTTAC 233

```

Search completed: May 24, 2003, 14:52:22
 Job time : 353.903 secs

GenCore version 5.1.4.p5.4578
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OM nucleic - nucleic search, using sw model

Run on: May 24, 2003, 07:18:51 ; Search time 108.726 Seconds
(without alignments)
1304.896 Million cell updates/sec

Title: US-09-963-803-11

Perfect score: 63

Sequence: 1 ggcggaagaacttatgc.....tgcgcgtcccaagcttat 63

Scoring table: IDENTITY_NUC

Gapop 10.0, Gapext 1.0

Searched: 2185239 seqs, 112599159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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2: /SID52/gcgdata/geneseq/geneseq-emb1/NA1981.DAT:*

3: /SID52/gcgdata/geneseq/geneseq-emb1/NA1982.DAT:*

4: /SID52/gcgdata/geneseq/geneseq-emb1/NA1983.DAT:*

5: /SID52/gcgdata/geneseq/geneseq-emb1/NA1984.DAT:*

6: /SID52/gcgdata/geneseq/geneseq-emb1/NA1985.DAT:*

7: /SID52/gcgdata/geneseq/geneseq-emb1/NA1986.DAT:*

8: /SID52/gcgdata/geneseq/geneseq-emb1/NA1987.DAT:*

9: /SID52/gcgdata/geneseq/geneseq-emb1/NA1988.DAT:*

10: /SID52/gcgdata/geneseq/geneseq-emb1/NA1989.DAT:*

11: /SID52/gcgdata/geneseq/geneseq-emb1/NA1990.DAT:*

12: /SID52/gcgdata/geneseq/geneseq-emb1/NA1991.DAT:*

13: /SID52/gcgdata/geneseq/geneseq-emb1/NA1992.DAT:*

14: /SID52/gcgdata/geneseq/geneseq-emb1/NA1993.DAT:*

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20: /SID52/gcgdata/geneseq/geneseq-emb1/NA1999.DAT:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	63	100.0	63	21	AAA96845
2	63	100.0	317	21	AAA96837
3	63	100.0	317	21	AAA96839
4	61.4	97.5	301	21	AAA96841
5	61.4	97.5	348	21	AAA96838
6	61.4	97.5	398	21	AAA96840
7	42	66.7	243	21	AAA96835
8	41.2	65.4	392	21	AAA96855
9	38.8	61.6	604	21	AAA96857

10	37	58.7	472	21	AAA96859	Nucleotide sequenc
11	37	58.7	541	21	AAA96858	Nucleotide sequenc
12	35.4	56.2	393	21	AAA96853	Nucleotide sequenc
13	35.4	56.2	462	21	AAA96854	Nucleotide sequenc
14	35.4	56.2	600	21	AAA96856	Nucleotide sequenc
15	24.8	39.4	434	24	ABL79935	Human ovarian canc
16	24.8	39.4	539	22	ABK68230	Human lung tumour
17	24.8	39.4	539	24	ABK38141	CDNA encoding clon
18	24.8	39.4	777	23	AA567507	DNA encoding novel
19	24.8	39.4	2551	9	AA81551	Bio F, Bio C and B
20	24.6	39.0	1449	21	AAC43051	Arabidopsis thalia
21	24.6	39.0	1506	21	AAC49145	Arabidopsis thalia
22	24	38.1	2765	23	ABL14808	Drosophila melanog
23	23.4	37.1	2413	24	ABNB8295	Human large protei
24	23.2	36.8	1461	22	AAH29763	S cerevisiae apopt
25	23.2	36.8	3411	23	ABL28884	Drosophila melanog
26	22.8	36.2	748	21	AAC44959	Arabidopsis thalia
27	22.8	36.2	888	21	AAC35439	Arabidopsis thalia
28	22.6	35.9	6565	23	ABL18414	Drosophila melanog
29	22.4	35.6	347	24	ABL82625	Human ovarian canc
30	22.4	35.6	12010	24	ABN96872	Gene #3370 used to
31	22.4	35.6	13857	22	AAK82827	Human immune/hema
32	22.2	35.2	220	21	AA445410	Human secreted exp
33	22.2	35.2	375	22	AAH52940	S. epidermidis ope
34	22.2	35.2	562	22	ABA09445	Human ICERB homolo
35	22.2	35.2	627	22	AAH52365	S. epidermidis ope
36	22.2	35.2	771	24	ABK75564	Bacillus lichenifo
37	22.2	35.2	841	22	AA15716	Human breast cance
38	22.2	35.2	1312	22	AA59199	Human MYO1 gene p
39	22.2	35.2	1330	21	AA16693	Human secreted pro
40	22.2	35.2	1563	21	AA236238	cDNA encoding a bo
41	22.2	35.2	1669	20	AA15104	High affinity immu
42	22.2	35.2	1670	21	AA232842	Human high affinity
43	22.2	35.2	1769	24	ABL90726	Human polynucleoti
44	22.2	35.2	2021	22	AA59183	Human MYO1 gene p
45	22.2	35.2	2284	22	AA59182	Human MYO1 gene p

ALIGNMENTS

RESULT 1	AAA96845	standard; DNA; 63 BP.
ID	AAA96845	
AC	AAA96845;	
XX		
DT	19-FEB-2001 (first entry)	
XX		
DE	Directional desoxynucleotide building block S4.	
XX		
KW	Promoter; intergenic region; Commelina yellow mottle virus;	
KW	Chimeric expression promoter; plant vascular expression promoter;	
KW	plant green tissue expression promoter; Cassava vein mosaic virus;	
KW	transgenic plant; ss.	
OS	Synthetic.	
XX		
PN	WO200058485-A1.	
XX		
PD	05-OCT-2000.	
XX		
PF	29-MAR-2000; 2000WO-IB00370.	
XX		
PR	29-MAR-1999; 99FR-0003925.	
XX		
PA	(MERI-) MERISTEM THERAPEUTICS.	
XX		
PI	Rance I, Gruber V, Theisen M;	
XX		
DR	WPI; 2000-647238/62.	
XX		
PT	Chimeric expression promoter for transgenic plant production, comprises	

PT sequence from promoter comprising vascular expression region replaced
PT with sequence from promoter comprising green tissue expression region
XX
XX Disclosure; Page 23; 91pp; English.
XX
CC The present sequence represents a directional desoxyribonucleotide building
CC block, which was used to construct chimeric promoters of the invention.
CC The specification describes chimeric expression promoters. These
CC chimeric promoters comprise a nucleic acid sequence which is derived
CC from a first plant promoter, in which a plant vascular expression
CC promoter region is replaced with a nucleic acid sequence derived from
CC a second plant promoter comprising a plant green tissue expression
CC promoter region. Preferably, the first plant promoter originates from
CC commelina yellow mottle virus, and the second plant promoter originates
CC from the cassava vein mosaic virus. Especially, the promoters are
CC derived from intergenic regions. The chimeric promoters are useful
CC for producing transgenic plants.
XX
SQ Sequence 63 BP; 14 A; 14 C; 15 G; 20 T; 0 other;
Query Match 100.0%; Score 63; DB 21; Length 63;
Best Local Similarity 100.0%; Pred. No. 2.8e-15;
Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GGGGGAAGTACCTTGTGATTTGTACTTGGTACCCTGATCCGGTTCCCACTT 60
DB 1 GGGGGAAGTACCTTGTGATTTGTACTTGGTACCCTGATCCGGTTCCCACTT 60
QY 61 TAT 63
DB 61 TAT 63
DB 61 TAT 63
RESULT 2
ID AAA96837 standard; DNA: 317 BP.
XX
AC AAA96837;
XX
DT 19-FEB-2001 (first entry)
XX
DE Nucleotide sequence of chimeric expression promoter MP1116.
XX
KW Promoter: intergenic region; Commelina yellow mottle virus;
KW chimeric expression promoter; plant vascular expression promoter;
KW plant green tissue expression promoter; Cassava vein mosaic virus;
KW transgenic plant; chimera; ss.
XX
OS Chimeric - Commelina yellow mottle virus.
OS Chimeric - Cassava vein mosaic virus.
XX
PN WO200058485-A1.
XX
PD 05-OCT-2000.
XX
PF 29-MAR-2000; 2000MO-IB00370.
XX
PR 29-MAR-1999; 99FR-0003925.
XX
PA (MERI-) MERISTEM THERAPEUTICS.
XX
PI Rance I, Gruber V, Theisen M;
XX
DR WPI; 2000-647238/62.
XX
PT Chimeric expression promoter for transgenic plant production, comprises
PT sequence from promoter comprising vascular expression region replaced
PT with sequence from promoter comprising green tissue expression region
XX
XX Claim 5; Page 81; 91pp; English.

CC The present sequence represents a chimeric promoter of the invention.
CC The specification describes chimeric expression promoters. These
CC chimeric promoters comprise a nucleic acid sequence which is derived
CC from a first plant promoter, in which a plant vascular expression
CC promoter region is replaced with a nucleic acid sequence derived from
CC a second plant promoter comprising a plant green tissue expression
CC promoter region. Preferably, the first plant promoter originates from
CC commelina yellow mottle virus, and the second plant promoter originates
CC from the cassava vein mosaic virus. Especially, the promoters are
CC derived from intergenic regions. The chimeric promoters are useful
CC for producing transgenic plants.
XX
SQ Sequence 317 BP; 107 A; 61 C; 74 G; 75 T; 0 other;
Query Match 100.0%; Score 63; DB 21; Length 317;
Best Local Similarity 100.0%; Pred. No. 3.9e-15;
Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GGGGGAAGTACCTTGTGATTTGTACTTGGTACCCTGATCCGGTTCCCACTT 60
DB 195 GGGGGAAGTACCTTGTGATTTGTACTTGGTACCCTGATCCGGTTCCCACTT 254
QY 61 TAT 63
DB 255 TAT 257
RESULT 3
ID AAA96839 standard; DNA: 371 BP.
XX
AC AAA96839;
XX
DT 19-FEB-2001 (first entry)
XX
DE Nucleotide sequence of chimeric expression promoter MP1146.
XX
KW Promoter: intergenic region; Commelina yellow mottle virus;
KW chimeric expression promoter; plant vascular expression promoter;
KW plant green tissue expression promoter; Cassava vein mosaic virus;
KW transgenic plant; chimera; ss.
XX
OS Chimeric - Commelina yellow mottle virus.
OS Chimeric - Cassava vein mosaic virus.
XX
PN WO200058485-A1.
XX
PD 05-OCT-2000.
XX
PF 29-MAR-2000; 2000MO-IB00370.
XX
PR 29-MAR-1999; 99FR-0003925.
XX
PA (MERI-) MERISTEM THERAPEUTICS.
XX
PI Rance I, Gruber V, Theisen M;
XX
DR WPI; 2000-647238/62.
XX
PT Chimeric expression promoter for transgenic plant production, comprises
PT sequence from promoter comprising vascular expression region replaced
PT with sequence from promoter comprising green tissue expression region
XX
XX Claim 5; Page 81; 91pp; English.
XX
CC The present sequence represents a chimeric promoter of the invention.
CC The specification describes chimeric expression promoters. These
CC chimeric promoters comprise a nucleic acid sequence which is derived
CC from a first plant promoter, in which a plant vascular expression
CC promoter region is replaced with a nucleic acid sequence derived from
CC a second plant promoter comprising a plant green tissue expression
CC promoter region. Preferably, the first plant promoter originates from
CC promoter region. Especially, the promoters are useful
CC for producing transgenic plants.

OY 61 TAT 63
 Db 288 TAT 290

RESULT 6
 AAA96840
 ID AAA96840 standard; DNA; 398 BP.

AC AAA96840;
 XX
 DT 19-FEB-2001 (first entry)

DE Nucleotide sequence of chimeric expression promoter MP1147.

XX Promoter; intergenic region; Commelina yellow mottle virus;
 KM chimeric expression promoter; plant vascular expression promoter;
 KM plant green tissue expression promoter; Cassava vein mosaic virus;
 KM transgenic plant; chimera; ss.

XX Chimeric - Commelina yellow mottle virus.
 OS Chimeric - Cassava vein mosaic virus.

XX MO200058485-A1.

PD 05-OCT-2000.

PF 29-MAR-2000; 2000WO-IB00370.

PR 29-MAR-1999; 99FR-0003925.

PA (MERI-) MERISTEM THERAPEUTICS.

PI Rance I, Gruber V, Theisen M;

XX WPI; 2000-647238/62.

XX Chimeric expression promoter for transgenic plant production, comprises
 PT sequence from promoter comprising vascular expression region replaced
 PT with sequence from promoter comprising green tissue expression region

XX Claim 5; Page 82; 91pp; English.

XX The present sequence represents a chimeric promoter of the invention.
 CC The specification describes chimeric expression promoters. These
 CC chimeric promoters comprise a nucleic acid sequence which is derived
 CC from a first plant promoter, in which a plant vascular expression
 CC promoter region is replaced with a nucleic acid sequence derived from
 CC a second plant promoter comprising a plant green tissue expression
 CC promoter region. Preferably, the first plant promoter originates from
 CC Commelina yellow mottle virus, and the second plant promoter originates
 CC from the Cassava vein mosaic virus. Especially, the promoters are
 CC derived from intergenic regions. The chimeric promoters are useful
 CC for producing transgenic plants.

XX Sequence 398 BP; 128 A; 80 C; 93 G; 97 T; 0 other;

Query Match 97.5%; Score 61.4; DB 21; Length 398;
 Best Local Similarity 98.4%; Pred. No. 1.7e-14;
 Matches 62; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 GGGGAAAGTAACTTATGCTTGAACCTGTCACCGGTATGCCGGTTCACCAAGCTT 60
 Db 278 GGGGAAAGTAACTTATGCTTGAACCTGTCACCGGTATGCCGGTTCACCAAGCTT 337

OY 61 TAT 63
 Db 338 TAT 340

RESULT 7

AAA96835
 ID AAA96835 standard; DNA; 243 BP.

AC AAA96835;

DT 19-FEB-2001 (first entry)

DE Promoter from intergenic region of Commelina yellow mottle virus.

XX Promoter; intergenic region; Commelina yellow mottle virus;
 KM chimeric expression promoter; plant vascular expression promoter;
 KM plant green tissue expression promoter; Cassava vein mosaic virus;
 KM transgenic plant; ss.

XX Commelina yellow mottle virus.

PN MO200058485-A1.

PD 05-OCT-2000.

PF 29-MAR-2000; 2000WO-IB00370.

PR 29-MAR-1999; 99FR-0003925.

PA (MERI-) MERISTEM THERAPEUTICS.

PI Rance I, Gruber V, Theisen M;

XX WPI; 2000-647238/62.

XX Chimeric expression promoter for transgenic plant production, comprises
 PT sequence from promoter comprising vascular expression region replaced
 PT with sequence from promoter comprising green tissue expression region

XX Claim 4; Page 79; 91pp; English.

XX The present sequence represents a promoter fragment from the intergenic
 CC region of Commelina yellow mottle virus. The promoter is a strong
 CC promoter in vascular and reproductive tissues. The promoter is used to
 CC construct chimeric expression promoters. These chimeric promoters
 CC comprise a nucleic acid sequence which is derived from a first
 CC plant promoter, in which a plant vascular expression promoter region is
 CC replaced with a nucleic acid sequence derived from a second plant
 CC promoter comprising a plant green tissue expression promoter region.
 CC Preferably, the first plant promoter originates from Commelina yellow
 CC mottle virus, and the second plant promoter originates from the Cassava
 CC vein mosaic virus. The chimeric promoters are useful for producing
 CC transgenic plants.

XX Sequence 243 BP; 71 A; 53 C; 45 G; 74 T; 0 other;

Query Match 66.7%; Score 42; DB 21; Length 243;
 Best Local Similarity 100.0%; Pred. No. 7.2e-07;
 Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 22 TTTGTAACTTGTATACCGGTATGCGGTTCACCAAGCTTAT 63
 Db 153 TTTGTAACTTGTATACCGGTATGCGGTTCACCAAGCTTAT 194

RESULT 8
 AAA96855
 ID AAA96855 standard; DNA; 392 BP.

AC AAA96855;

DT 19-FEB-2001 (first entry)

DE Nucleotide sequence of chimeric expression promoter MP1164.

XX Promoter; intergenic region; Commelina yellow mottle virus;
 KM chimeric expression promoter; plant vascular expression promoter;

KW plant green tissue expression promoter; Cassava vein mosaic virus;
 XX transgenic plant; chimera; ss.
 OS Chimeric - Commelina yellow mottle virus.
 OS Chimeric - Cassava vein mosaic virus.
 XX
 PN WO200058485-A1.
 XX
 PD 05-OCT-2000.
 XX
 PF 29-MAR-2000; 2000WO-IB00370.
 XX
 PR 29-MAR-1999; 99FR-0003925.
 XX
 PA (MERI-) MERISTEM THERAPEUTICS.
 XX
 PI Rance I, Gruber V, Theisen M;
 XX
 DR WPI: 2000-647238/62.
 XX
 PT Chimeric expression promoter for transgenic plant production, comprises
 PT sequence from promoter comprising vascular expression region replaced
 PT with sequence from promoter comprising green tissue expression region
 XX
 PS Claim 5; Page 86; 91pp; English.
 XX
 CC The present sequence represents a chimeric promoter of the invention.
 CC The specification describes chimeric expression promoters. These
 CC chimeric promoters comprise a nucleic acid sequence which is derived
 CC from a first plant promoter, in which a plant vascular expression
 CC promoter region is replaced with a nucleic acid sequence derived from
 CC a second plant promoter comprising a plant green tissue expression
 CC promoter region. Preferably, the first plant promoter originates from
 CC Commelina yellow mottle virus, and the second plant promoter originates
 CC from the Cassava vein mosaic virus. Especially, the promoters are
 CC derived from intergenic regions. The chimeric promoters are useful
 CC for producing transgenic plants.
 CC
 SQ Sequence 392 BP; 127 A; 80 C; 87 G; 98 T; 0 other;
 XX
 Query Match 65.4%; Score 41.2; DB 21; Length 392;
 Best Local Similarity 79.0%; Pred. No. 1.6e-06;
 Matches 49; Conservative 0; Mismatches 13; Indels 0; Gaps 0;
 OY 1 GCGGAAAGTACCTTATGCAATTGTGTAAGTACCGGATGCGGTTCCCAAGCT 60
 DB 197 GCGGAAAGTACCTTATGCAATTGTGTAAGTACCGGATGCGGTTCCCAAGCT 256
 OY 61 TA 62
 DB 257 CA 258
 XX
 AC AAA96857;
 XX
 DT 19-FEB-2001 (first entry)
 XX
 DE Nucleotide sequence of chimeric expression promoter MPr1167.
 XX
 KW Promoter; intergenic region; Commelina yellow mottle virus;
 KW chimeric expression promoter; plant vascular expression promoter;
 KW plant green tissue expression promoter; Cassava vein mosaic virus;
 KW transgenic plant; chimera; ss.
 XX
 OS Chimeric - Commelina yellow mottle virus.
 OS Chimeric - Cassava vein mosaic virus.
 XX
 PN WO200058485-A1.

XX
 PD 05-OCT-2000.
 XX
 PF 29-MAR-2000; 2000WO-IB00370.
 XX
 PR 29-MAR-1999; 99FR-0003925.
 XX
 PA (MERI-) MERISTEM THERAPEUTICS.
 XX
 PI Rance I, Gruber V, Theisen M;
 XX
 DR WPI: 2000-647238/62.
 XX
 PT Chimeric expression promoter for transgenic plant production, comprises
 PT sequence from promoter comprising vascular expression region replaced
 PT with sequence from promoter comprising green tissue expression region
 XX
 PS Claim 5; Page 87; 91pp; English.
 XX
 CC The present sequence represents a chimeric promoter of the invention.
 CC The specification describes chimeric expression promoters. These
 CC chimeric promoters comprise a nucleic acid sequence which is derived
 CC from a first plant promoter, in which a plant vascular expression
 CC promoter region is replaced with a nucleic acid sequence derived from
 CC a second plant promoter comprising a plant green tissue expression
 CC promoter region. Preferably, the first plant promoter originates from
 CC Commelina yellow mottle virus, and the second plant promoter originates
 CC from the Cassava vein mosaic virus. Especially, the promoters are
 CC derived from intergenic regions. The chimeric promoters are useful
 CC for producing transgenic plants.
 CC
 SQ Sequence 604 BP; 186 A; 116 C; 145 G; 157 T; 0 other;
 XX
 Query Match 61.6%; Score 38.8; DB 21; Length 604;
 Best Local Similarity 95.2%; Pred. No. 1.6e-05;
 Matches 40; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 OY 1 GCGGAAAGTACCTTATGCAATTGTGTAAGTACCGGATGCGGTTCCCAAGCT 42
 DB 278 GCGGAAAGTACCTTATGCAATTGTGTAAGTACCGGATGCGGTTCCCAAGCT 319
 OY
 DB
 XX
 AC AAA96859;
 XX
 DT 19-FEB-2001 (first entry)
 XX
 DE Nucleotide sequence of chimeric expression promoter MPr1169.
 XX
 KW Promoter; intergenic region; Commelina yellow mottle virus;
 KW chimeric expression promoter; plant vascular expression promoter;
 KW plant green tissue expression promoter; Cassava vein mosaic virus;
 KW transgenic plant; chimera; ss.
 XX
 OS Chimeric - Commelina yellow mottle virus.
 OS Chimeric - Cassava vein mosaic virus.
 XX
 PN WO200058485-A1.
 XX
 PD 05-OCT-2000.
 XX
 PF 29-MAR-2000; 2000WO-IB00370.
 XX
 PR 29-MAR-1999; 99FR-0003925.
 XX
 PA (MERI-) MERISTEM THERAPEUTICS.
 XX
 PI Rance I, Gruber V, Theisen M;
 XX

DR WPI; 2000-647238/62.
 XX
 PT Chimeric expression promoter for transgenic plant production, comprises
 PT sequence from promoter comprising vascular expression region replaced
 PT with sequence from promoter comprising green tissue expression region
 PT
 XX
 PS Claim 5; Page 88; 91pp; English.
 XX
 CC The present sequence represents a chimeric promoter of the invention.
 CC The specification describes chimeric expression promoters. These
 CC chimeric promoters comprise a nucleic acid sequence which is derived
 CC from a first plant promoter, in which a plant vascular expression
 CC promoter region is replaced with a nucleic acid sequence derived from
 CC a second plant promoter comprising a plant green tissue expression
 CC promoter region. Preferably, the first plant promoter originates from
 CC Comelina yellow mottle virus, and the second plant promoter originates
 CC from the Cassava vein mosaic virus. Especially, the promoters are
 CC derived from intergenic regions. The chimeric promoters are useful
 CC for producing transgenic plants.
 XX
 SQ Sequence 472 BP; 149 A; 92 C; 112 G; 119 T; 0 other;
 XX
 Query Match 58.7%; Score 37; DB 21; Length 472;
 Best Local Similarity 100.0%; Pred. No. 7.8e-05;
 Matches 37; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GCGGGAAGTACCTTATGCACTTGTACTGCTTAC 37
 DB 278 GCGGGAAGTACCTTATGCACTTGTACTGCTTAC 314
 ID AAA96858 standard; DNA; 541 BP.
 XX
 AC AAA96858;
 XX
 DT 19-FEB-2001 (first entry)
 XX
 DE Nucleotide sequence of chimeric expression promoter MP1168.
 XX
 KW Promoter: intergenic region; Comelina yellow mottle virus;
 KW chimeric expression promoter; plant vascular expression promoter;
 KW plant green tissue expression promoter; Cassava vein mosaic virus;
 KW transgenic plant; chimera; ss.
 XX
 OS Chimeric - Comelina yellow mottle virus.
 OS Chimeric - Cassava vein mosaic virus.
 XX
 PN WO200058485-A1.
 XX
 PD 05-OCT-2000.
 XX
 PF 29-MAR-2000; 2000MO-IB00370.
 XX
 PR 29-MAR-1999; 99FR-0003925.
 XX
 PA (MERI-) MERISTEM THERAPEUTICS.
 XX
 PI Rance I, Gruber V, Theisen M;
 XX
 DR WPI; 2000-647238/62.
 XX
 PT Chimeric expression promoter for transgenic plant production, comprises
 PT sequence from promoter comprising vascular expression region replaced
 PT with sequence from promoter comprising green tissue expression region
 PT
 XX
 PS Claim 5; Page 87-88; 91pp; English.
 XX
 CC The present sequence represents a chimeric promoter of the invention.
 CC The specification describes chimeric expression promoters. These

CC chimeric promoters comprise a nucleic acid sequence which is derived
 CC from a first plant promoter, in which a plant vascular expression
 CC promoter region is replaced with a nucleic acid sequence derived from
 CC a second plant promoter comprising a plant green tissue expression
 CC promoter region. Preferably, the first plant promoter originates from
 CC Comelina yellow mottle virus, and the second plant promoter originates
 CC from the Cassava vein mosaic virus. Especially, the promoters are
 CC derived from intergenic regions. The chimeric promoters are useful
 CC for producing transgenic plants.
 XX
 SQ Sequence 541 BP; 169 A; 104 C; 130 G; 138 T; 0 other;
 XX
 Query Match 58.7%; Score 37; DB 21; Length 541;
 Best Local Similarity 100.0%; Pred. No. 8e-05;
 Matches 37; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GCGGGAAGTACCTTATGCACTTGTACTGCTTAC 37
 DB 278 GCGGGAAGTACCTTATGCACTTGTACTGCTTAC 314
 ID AAA96853 standard; DNA; 393 BP.
 XX
 AC AAA96853;
 XX
 DT 19-FEB-2001 (first entry)
 XX
 DE Nucleotide sequence of chimeric expression promoter MP1162.
 XX
 KW Promoter: intergenic region; Comelina yellow mottle virus;
 KW chimeric expression promoter; plant vascular expression promoter;
 KW plant green tissue expression promoter; Cassava vein mosaic virus;
 KW transgenic plant; chimera; ss.
 XX
 OS Chimeric - Comelina yellow mottle virus.
 OS Chimeric - Cassava vein mosaic virus.
 XX
 PN WO200058485-A1.
 XX
 PD 05-OCT-2000.
 XX
 PF 29-MAR-2000; 2000MO-IB00370.
 XX
 PR 29-MAR-1999; 99FR-0003925.
 XX
 PA (MERI-) MERISTEM THERAPEUTICS.
 XX
 PI Rance I, Gruber V, Theisen M;
 XX
 DR WPI; 2000-647238/62.
 XX
 PT Chimeric expression promoter for transgenic plant production, comprises
 PT sequence from promoter comprising vascular expression region replaced
 PT with sequence from promoter comprising green tissue expression region
 PT
 XX
 PS Claim 5; Page 85; 91pp; English.
 XX
 CC The present sequence represents a chimeric promoter of the invention.
 CC The specification describes chimeric expression promoters. These
 CC chimeric promoters comprise a nucleic acid sequence which is derived
 CC from a first plant promoter, in which a plant vascular expression
 CC promoter region is replaced with a nucleic acid sequence derived from
 CC a second plant promoter comprising a plant green tissue expression
 CC promoter region. Preferably, the first plant promoter originates from
 CC Comelina yellow mottle virus, and the second plant promoter originates
 CC from the Cassava vein mosaic virus. Especially, the promoters are
 CC derived from intergenic regions. The chimeric promoters are useful
 CC for producing transgenic plants.
 XX
 SQ Sequence 393 BP; 128 A; 75 C; 93 G; 97 T; 0 other;

Query Match 56.2%; Score 35.4; DB 21; Length 393;
Best Local Similarity 97.3%; Pred. No. 0.00032;
Matches 36; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 GCGGAAAGTACCTTATGCACTTGTGTTAC 37
DB 197 GCGGAAAGTACCTTATGCACTTGTGTTAC 233

RESULT 13
AAA96854
ID AAA96854 standard; DNA; 462 BP.

XX AAA96854;

XX 19-FEB-2001 (first entry)

DE Nucleotide sequence of chimeric expression promoter MP1163.

XX Promoter; intergenic region; Commelina yellow mottle virus;

KM chimeric expression promoter; plant vascular expression promoter;

KW plant green tissue expression promoter; Cassava vein mosaic virus;

XX transgenic plant; chimera; ss.

OS Chimeric - Commelina yellow mottle virus.

XX Chimeric - Cassava vein mosaic virus.

XX WO200058485-A1.

XX 05-OCT-2000.

XX 29-MAR-2000; 2000WO-IB00370.

XX 29-MAR-1999; 99FR-0003925.

XX (MERI-) MERISTEM THERAPEUTICS.

XX Rance I, Gruber V, Theisen M;

XX WPI; 2000-647238/62.

XX Chimeric expression promoter for transgenic plant production, comprises

XX sequence from promoter comprising vascular expression region replaced

XX with sequence from promoter comprising green tissue expression region

XX Claim 5; Page 86; 91pp; English.

XX The present sequence represents a chimeric promoter of the invention.

XX The specification describes chimeric expression promoters. These

XX chimeric promoters comprise a nucleic acid sequence which is derived

XX from a first plant promoter, in which a plant vascular expression

XX promoter region is replaced with a nucleic acid sequence derived from

XX a second plant promoter comprising a plant green tissue expression

XX promoter region. Preferably, the first plant promoter originates from

XX Commelina yellow mottle virus, and the second plant promoter originates

XX from the Cassava vein mosaic virus. Especially, the promoters are

XX derived from intergenic regions. The chimeric promoters are useful

XX for producing transgenic plants.

AAA96856
ID AAA96856 standard; DNA; 600 BP.

XX AAA96856;

XX 19-FEB-2001 (first entry)

DE Nucleotide sequence of chimeric expression promoter MP1165.

XX Promoter; intergenic region; Commelina yellow mottle virus;

KM chimeric expression promoter; plant vascular expression promoter;

KW plant green tissue expression promoter; Cassava vein mosaic virus;

XX transgenic plant; chimera; ss.

OS Chimeric - Commelina yellow mottle virus.

XX Chimeric - Cassava vein mosaic virus.

XX WO200058485-A1.

XX 05-OCT-2000.

XX 29-MAR-2000; 2000WO-IB00370.

XX 29-MAR-1999; 99FR-0003925.

XX (MERI-) MERISTEM THERAPEUTICS.

XX Rance I, Gruber V, Theisen M;

XX WPI; 2000-647238/62.

XX Chimeric expression promoter for transgenic plant production, comprises

XX sequence from promoter comprising vascular expression region replaced

XX with sequence from promoter comprising green tissue expression region

XX Claim 5; Page 86-87; 91pp; English.

XX The present sequence represents a chimeric promoter of the invention.

XX The specification describes chimeric expression promoters. These

XX chimeric promoters comprise a nucleic acid sequence which is derived

XX from a first plant promoter, in which a plant vascular expression

XX promoter region is replaced with a nucleic acid sequence derived from

XX a second plant promoter comprising a plant green tissue expression

XX promoter region. Preferably, the first plant promoter originates from

XX Commelina yellow mottle virus, and the second plant promoter originates

XX from the Cassava vein mosaic virus. Especially, the promoters are

XX derived from intergenic regions. The chimeric promoters are useful

XX for producing transgenic plants.

XX Sequence 600 BP; 188 A; 111 C; 147 G; 154 T; 0 other;

XX Query Match 56.2%; Score 35.4; DB 21; Length 600;

XX Best Local Similarity 97.3%; Pred. No. 0.00035;

XX Matches 36; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

XX OY 1 GCGGAAAGTACCTTATGCACTTGTGTTAC 37
DB 197 GCGGAAAGTACCTTATGCACTTGTGTTAC 233

RESULT 15

ABL79935/C

ID ABL79935 standard; CDNA; 434 BP.

XX ABL79935;

XX 17-MAY-2002 (first entry)

XX Human ovarian cancer related CDNA clone SEQ ID NO:2913.

XX Human; ovarian cancer; ovarian tumour; cytostatic; gene; ss.

XX

```
OS Homo sapiens.
XX
PN WO200192581-A2.
XX
PD 06-DEC-2001.
XX
PF 29-MAY-2001; 2001WO-US17756.
XX
PR 26-MAY-2000; 2000US-207484P.
XX
PA (CORI-) CORIXA CORP.
XX
PI Algate PA, Harlocker SL, Jones R;
XX
DR WPI; 2002-122075/16.
XX
PT Composition for therapy and diagnosis of ovarian cancer comprising
PT polypeptide of a ovarian tumor polypeptide, polynucleotide encoding
PT polypeptide, antibody specific to polypeptide or T cell expressing
PT polypeptide
XX
PS Claim 1; SEQ ID 2913; 4899p; English.
XX
CC The present invention describes a composition (I) comprising: carriers
CC and immunostimulants; and a polypeptide (II) of a ovarian tumor
CC polypeptide encoded by a polynucleotide (III) having a cDNA sequence
CC (S1) from the 10912 nucleotide sequences as given in ABL77023 to
CC ABL87934, (III) encoding (II) having a sequence (S2), a T cell
CC population of (II), or antigen presenting cells that express (II).
CC (I) has cytostatic activity. An oligonucleotide (IV) that hybridises to
CC (S1) can be used for detecting ovarian cancer in a patient's biological
CC sample preferably serum or ovarian tissue. The method comprises
CC contacting a biological sample from a patient with (IV), detecting the
CC amount of polynucleotide hybridising to (IV) and comparing the amount to
CC a predetermined cutoff value and thereby detecting ovarian cancer in the
CC patient, where the amount of polynucleotide hybridising to (IV) is
CC detected preferably by polymerase chain reaction (PCR). (I) comprising
CC (III) and/or (II) is useful for stimulating and/or expanding T cells
CC specific for an ovarian tumor protein comprising contacting T cells
CC with (III) or (II). (III) is useful in design and preparation of
CC ribozyme molecules for inhibiting expression of the tumour polypeptides
CC and proteins in tumour cells; and to isolate a full length gene from a
CC suitable library e.g., a tumour cDNA library using well known
CC techniques.
XX
SQ Sequence 434 BP; 136 A; 66 C; 92 G; 140 T; 0 other;
XX
Query Match 39.4%; Score 24.8; DB 24; Length 434;
Best Local Similarity 63.3%; Pred. No. 5;
Matches 38; Conservative 0; Mismatches 22; Indels 0; Gaps 0;
OY 4 GGAAGTACCTTATGCACTTGTAACTGCTACCGGTATGCCGGTTCACCAAGCTTAT 63
DB 92 GGTATAGCAATGTCATTTGTTACTGCTGCTTCTAGATCAACCTTACACAGCTATAT 33
Search completed: May 24, 2003, 14:34:43
Job time : 110.726 secs
```

GenCore version 5.1.4.p5.4578
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OM nucleic - nucleic search, using sw model

Run on: May 24, 2003, 13:52:01 ; Search time 26.0806 Seconds
(without alignments)
740.804 Million cell updates/sec

Title: US-09-963-803-11

Sequence: 1 ggcggaaagtaacctatgc.....tgccggttcccaagctttat 63

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 441362 seqs, 153338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database : Issued_Patents_NA:*

1: /cgn2_6/prodata/1/ina/5A.COMB.seq:.*
2: /cgn2_6/prodata/1/ina/5B.COMB.seq:.*
3: /cgn2_6/prodata/1/ina/6A.COMB.seq:.*
4: /cgn2_6/prodata/1/ina/6B.COMB.seq:.*
5: /cgn2_6/prodata/1/ina/PCUTS.COMB.seq:.*
6: /cgn2_6/prodata/1/ina/backfiles1.seq:.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	22.2	35.2	1312	4 US-09-193-792-20	Sequence 20, Appl
C 2	22.2	35.2	1669	2 US-08-916-902A-2	Sequence 2, Appl
C 3	22.2	35.2	1669	2 US-09-213-389-2	Sequence 2, Appl
C 4	22.2	35.2	2021	4 US-09-193-792-2	Sequence 2, Appl
C 5	22.2	35.2	2284	4 US-09-193-792-1	Sequence 1, Appl
C 6	22.2	35.2	3140	4 US-08-961-527-158	Sequence 18, Appl
C 7	21.8	34.6	6082	4 US-09-605-785-535	Sequence 535, App
C 8	21.8	34.6	6082	4 US-09-439-313-535	Sequence 535, App
C 9	21.8	34.6	6140	4 US-09-605-785-536	Sequence 536, App
C 10	21.8	34.6	6140	4 US-09-439-313-536	Sequence 536, App
C 11	21.2	33.7	3611	2 US-08-727-118-1	Sequence 1, Appl
C 12	20.8	33.0	2233	3 US-08-680-506-4	Sequence 4, Appl
C 13	20.8	33.0	5077	3 US-08-680-506-2	Sequence 4, Appl
C 14	20.8	33.0	8321	3 US-08-680-506-1	Sequence 1, Appl
C 15	20.8	33.0	12124	1 US-08-181-271A-36	Sequence 36, Appl
C 16	20.8	33.0	12124	1 US-08-449-315-36	Sequence 36, Appl
C 17	20.8	33.0	12124	1 US-08-444-803-36	Sequence 36, Appl
C 18	20.8	33.0	12124	1 US-08-449-043-36	Sequence 36, Appl
C 19	20.8	33.0	12124	1 US-08-456-265A-36	Sequence 36, Appl
C 20	20.8	33.0	12124	1 US-08-455-416-36	Sequence 36, Appl
C 21	20.8	33.0	12124	1 US-08-455-244-36	Sequence 36, Appl
C 22	20.8	33.0	12124	1 US-08-454-876-36	Sequence 36, Appl
C 23	20.8	33.0	12124	2 US-08-457-364-36	Sequence 36, Appl
C 24	20.8	33.0	12124	2 US-08-456-262-36	Sequence 36, Appl
C 25	20.8	33.0	12124	2 US-08-456-240-36	Sequence 36, Appl
C 26	20.8	33.0	12124	2 US-08-455-736-36	Sequence 36, Appl
C 27	20.8	33.0	12124	2 US-08-971-217-36	Sequence 36, Appl

C 28	20.8	33.0	12124	4 US-09-350-600-36	Sequence 36, Appl
C 29	20.8	33.0	41708	4 US-09-470-512A-3	Sequence 3, Appl
C 30	20.6	32.7	648	4 US-09-134-001C-458	Sequence 458, App
C 31	20.6	32.7	1275	4 US-09-134-001C-2388	Sequence 2388, App
C 32	20.6	32.7	1551	4 US-09-134-001C-567	Sequence 567, App
C 33	20.6	32.7	4223	4 US-08-845-258-7	Sequence 7, Appl
C 34	20.6	32.7	4223	4 US-08-845-258-45	Sequence 45, Appl
C 35	20.6	32.7	4223	4 US-08-990-571-7	Sequence 7, Appl
C 36	20.6	32.7	4223	4 US-08-990-571-45	Sequence 45, Appl
C 37	20.6	32.7	4223	4 US-08-723-142A-7	Sequence 7, Appl
C 38	20.6	32.7	4223	4 US-08-723-142A-45	Sequence 45, Appl
C 39	20.6	32.7	4223	4 US-09-528-784A-7	Sequence 7, Appl
C 40	20.6	32.7	4223	4 US-09-528-784A-45	Sequence 45, Appl
C 41	20.6	32.7	5912	2 US-08-629-001A-1	Sequence 1, Appl
C 42	20.6	32.7	5912	4 US-08-642-274D-1	Sequence 1, Appl
C 43	20.6	32.7	5912	4 US-08-952-127-1	Sequence 1, Appl
C 44	20.6	32.7	5912	4 US-08-952-014C-1	Sequence 1, Appl
C 45	20.6	32.7	6525	1 US-08-493-092-3	Sequence 3, Appl

ALIGNMENTS

```
RESULT 1
US-09-193-792-20/c
: Sequence 20, Application US/09193792B
: Patent No. 6180344
: GENERAL INFORMATION:
: APPLICANT: Chen, Bin
: TITLE OF INVENTION: 5' Upstream Region Sequences of the MYO1 Gene
: FILE REFERENCE: D6015
: CURRENT APPLICATION NUMBER: US/09/193,792B
: PRIOR FILING DATE: 1998-11-17
: PRIOR APPLICATION NUMBER: US 60/065,113
: NUMBER OF SEQ ID NOS: 20
: SEQ ID NO 20
: LENGTH: 1312
: TYPE: DNA
: ORGANISM: Homo sapiens
: FEATURE:
: OTHER INFORMATION: Pcti-Ehei fragment (Pcti.3) inserted in the multiple
: OTHER INFORMATION: cloning region of a pcle enhancer vector to construct
: OTHER INFORMATION: the transfection plasmid
US-09-193-792-20
Query Match 35.2%, Score 22.2; DB 4; Length 1312;
Best Local Similarity 64.7%, Pred. No. 9.4;
Matches 33; Conservative 0; Mismatches 18; Indels 0; Gaps 0;
Oy 11 AACCTTATGCAATTTGTACTGTTGATCCCGGATCCGCTTCCCAAGCTTT 61
Db 1091 AGCCTTAGCGGCTGACACTTGGCTCTCCGGACGCCCTTCCCAACTCT 1041
RESULT 2
US-08-916-902A-2
: Sequence 2, Application US/08916902A
: Patent No. 5871930
: GENERAL INFORMATION:
: APPLICANT: Bandman, Olga
: APPLICANT: Lal, Preeti
: APPLICANT: Corley, Neil C.
: TITLE OF INVENTION: HIGH AFFINITY IMMUNOGLOBULIN E
: TITLE OF INVENTION: RECEPTOR-LIKE PROTEIN
: NUMBER OF SEQUENCES: 4
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Incyte Pharmaceuticals, Inc.
: STREET: 3174 Porter Drive
: CITY: Palo Alto
: STATE: CA
: COUNTRY: USA
```

```

      : REGISTRATION NUMBER: 36,749
      : REFERENCE/DOCKET NUMBER: PF-0371 US
      : TELECOMMUNICATION INFORMATION:
      : TELEPHONE: 415-855-0555
      : TELEFAX: 415-845-4166
      : TELEX:
      : INFORMATION FOR SEQ ID NO: 2:
      : SEQUENCE CHARACTERISTICS:
      : LENGTH: 1669 base pairs
      : TYPE: nucleic acid
      : STRANDEDNESS: single
      : TOPOLOGY: linear
      : IMMEDIATE SOURCE:
      : LIBRARY: BRAINMOT04
      : CLONE: 927955
      :
      : US-09-213-389-2

```

```

Query Match          35.2%; Score 22.2; DB 2; Length 1669;
Best Local Similarity 61.0%; Pred. No. 10;
Matches    36; Conservative 0; Mismatches   23; Indels    0; Gaps    0;

```

```

Oy      5 GAAGATTAACCTGATTCATTGTGAAGTTGGTATCCCGGTATGCCGGTTCACAAGCTTAT 63
       | ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db     435 GGAAGTAAACCCTAATTTCCGCTGATATCGGGTACACAAATTTGGGGGGCATATAATGTTAT 493

```

RESULT 4
 US-09-193-792-2/c
 : Sequence 2, Application US/09193792B
 : Patent No. 6180344
 : GENERAL INFORMATION:
 : APPLICANT: Chen, Bin
 : TITLE OF INVENTION: 5 (Upstream Region Sequences of the MYOD1 Gene
 : TITLE OF INVENTION: and Uses Thereof
 : FILE REFERENCE: D6015
 : CURRENT APPLICATION NUMBER: US/09/193,792B
 : CURRENT FILING DATE: 1998-11-17
 : PRIOR APPLICATION NUMBER: US 60/065,113
 : PRIOR FILING DATE: 1997-11-18
 : NUMBER OF SEQ ID NOS: 20
 : SEQ ID NO 2
 : LENGTH: 2021
 : TYPE: DNA
 : ORGANISM: Homo sapiens
 : FEATURE:
 : OTHER INFORMATION: PstI fragment (Pp2.0) used as a hybridization probe
 : US-09-193-792-2

```

Query Match 35.2%; Score 22.2; DB 4; Length 2021;
Best Local Similarity 64.7%; Pred. No. 10;
Matches 33; Conservative 0; Mismatches 18; Indels 0; Gaps 0;

QY      11 AACCTTAGCATTTGTGTAACCTTGTTACCGCGTATGCGCGTTCCAGACTTT 61
      1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
Db      1091 AGCCTTAGCGCGCTGACACTTGCGTCTCGCGACGCGCTTTCCAAACCTCT 1041

RESULT 5
US-09-193-792-1/c
: Sequence 1, Application US/09193792B
: Patent No. 6180344
: GENERAL INFORMATION:
: APPLICANT: Chen, Bin
: TITLE OF INVENTION: 5 (Upstream Region Sequences of the MYOD) Gene
: TITLE OF INVENTION: and Uses Thereof
: FILE REFERENCE: D6015
: CURRENT APPLICATION NUMBER: US/09/193,792B
: CURRENT FILING DATE: 1998-11-17
: PRIOR APPLICATION NUMBER: US 60/065,113
: PRIOR FILING DATE: 1997-11-18
: NUMBER OF SEQ ID NOS: 20
: SEQ ID NO 1
: LENGTH: 2284

```


TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: promoter
LOCATION: -1537..747
OTHER INFORMATION: 5' upstream promoter region of the human MYO1 gene
US-09-193-792-1

Query Match 35.2%; Score 22.2; DB 4; Length 2284;
Best Local Similarity 64.7%; Pred. No. 11;
Matches 33; Conservative 0; Mismatches 18; Indels 0; Gaps 0;

QY 11 AACCTATGACATTTGATGTTACCGGATGCGGTTCCCAAGCTTT 61
DB 1210 AGCCCTAGCGGCTGACACTTGGCTCCGCGACGCGCTTCCAAACCTCT 1160

RESULT 6
US-08-961-527-158/C
Sequence 158, Application US/08961527
Patent No. 6420135
GENERAL INFORMATION:
APPLICANT: Charles Kunsch
TITLE OF INVENTION: Streptococcus pneumoniae polynucleotides and sequences
NUMBER OF SEQUENCES: 391
CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
STATE: Maryland
COUNTRY: USA
ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 Inch, 1.4Mb storage
OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCII text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/961,527
FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Brookes, A. Anders
REGISTRATION NUMBER: 36,373
REFERENCE/DOCKET NUMBER: PB340P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
TELEFAX: (301) 309-8512
INFORMATION FOR SEQ ID NO: 158:
SEQUENCE CHARACTERISTICS:
LENGTH: 3140 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
US-08-961-527-158

Query Match 35.2%; Score 22.2; DB 4; Length 3140;
Best Local Similarity 64.7%; Pred. No. 12;
Matches 33; Conservative 0; Mismatches 18; Indels 0; Gaps 0;

QY 3 CGGAAGTATGATGATTTGTTACCGGATGCGGTTCC 53
DB 1897 CGAATCATAGAAATATTCGTTGAACCTTGGTACGACAGATATGGGATTC 1847

RESULT 7
US-09-605-785-535/C
Sequence 535, Application US/09605785
Patent No. 6321716
GENERAL INFORMATION:

APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Jiang, Yugu
APPLICANT: Henderson, Robert A.
APPLICANT: Kalos, Michael D.
APPLICANT: Fanger, Gary R.
APPLICANT: Retter, Marc W.
APPLICANT: Stolk, John A.
APPLICANT: Day, Craig H.
APPLICANT: Vedvick, Thomas S.
APPLICANT: Carter, Darick
APPLICANT: Li, Samuel
APPLICANT: Wang, Aljun
APPLICANT: Skeiky, Yasir A.W.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE REFERENCE: 210121.427C16
CURRENT APPLICATION NUMBER: US/09/605,785
NUMBER OF SEQ ID NOS: 835
SOFTWARE: FASTSEQ for Windows Version 3.0
SEQ ID NO 535
LENGTH: 6082
TYPE: DNA
ORGANISM: Homo sapiens
US-09-605-785-535

Query Match 34.6%; Score 21.8; DB 4; Length 6082;
Best Local Similarity 61.4%; Pred. No. 19;
Matches 35; Conservative 0; Mismatches 22; Indels 0; Gaps 0;

QY 6 AAAGTACCTTATGATTTGTTACTGTTGTTACCGGATGCGGTTCCCAACTTTA 62
DB 2431 ACAGTACATTTAGCATTTGTTGTTGCCAGTATGAAGCACCAACTTGA 2375

RESULT 8
US-09-439-313-535/C
Sequence 535, Application US/09439313
Patent No. 6329505
GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan Louise
APPLICANT: Jiang, Yugu
APPLICANT: Reed, Steven G.
APPLICANT: Kalos, Michael
APPLICANT: Fanger, Gary
APPLICANT: Retter, Mark
APPLICANT: Solk, John
APPLICANT: Day, Craig
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE REFERENCE: 210121.427C9
CURRENT APPLICATION NUMBER: US/09/439,313
NUMBER OF SEQ ID NOS: 575
SOFTWARE: FASTSEQ for Windows Version 3.0
SEQ ID NO 535
LENGTH: 6082
TYPE: DNA
ORGANISM: Homo sapiens
US-09-439-313-535

Query Match 34.6%; Score 21.8; DB 4; Length 6082;
Best Local Similarity 61.4%; Pred. No. 19;
Matches 35; Conservative 0; Mismatches 22; Indels 0; Gaps 0;

QY 6 AAAGTACCTTATGATTTGTTACTGTTGTTACCGGATGCGGTTCCCAACTTTA 62

Db 2431 ACAGTGACATTAGCACTTTGTTGTTGCCAGTATGAAGCCACCAATCTTGA 2375

RESULT 9

US-09-605-785-536/C
Sequence 536, Application US/09605785
Patent No. 6321716

GENERAL INFORMATION:

APPLICANT: Xu, Jlangchun
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Jiang, Yuqul
APPLICANT: Henderson, Robert A.
APPLICANT: Kalos, Michael D.
APPLICANT: Fanger, Gary R.
APPLICANT: Retter, Marc W.
APPLICANT: Stolk, John A.
APPLICANT: Day, Craig H.
APPLICANT: Vedvick, Thomas S.
APPLICANT: Carter, Derrick
APPLICANT: Li, Samuel
APPLICANT: Wang, Aijun
APPLICANT: Skelky, Yasir A.W.
APPLICANT: Hepler, William
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE REFERENCE: 210121.427C16
CURRENT APPLICATION NUMBER: US/09/605,785
NUMBER OF SEQ ID NOS: 835
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 536
LENGTH: 6140
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: unsure
LOCATION: (4535)
OTHER INFORMATION: n-A,T,C or G
US-09-605-785-536

Query Match 34.6%; Score 21.8; DB 4; Length 6140;
Best Local Similarity 61.4%; Pred. No. 20;
Matches 35; Conservative 0; Mismatches 22; Indels 0; Gaps 0;

QY 6 AAGTACCTTATGCACTTTGTTACTGTTACCGGATGCCGTTCCCAAGCTTTA 62

Db 2405 ACAGTGACATTAGCACTTTGTTGTTGCCAGTATGAAGCCACCAATCTTGA 2349

RESULT 10

US-09-439-313-536/C
Sequence 536, Application US/09439313
Patent No. 6329505

GENERAL INFORMATION:

APPLICANT: Xu, Jlangchun
APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan Louise
APPLICANT: Jiang Yuqul
APPLICANT: Reed, Steven G.
APPLICANT: Kalos, Michael
APPLICANT: Fanger, Gary
APPLICANT: Retter, Mark
APPLICANT: Solk, John
APPLICANT: Day, Craig
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE REFERENCE: 210121.427C9
CURRENT APPLICATION NUMBER: US/09/439,313
CURRENT FILING DATE: 1999-11-12

NUMBER OF SEQ ID NOS: 575
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 536
LENGTH: 6140
TYPE: DNA
ORGANISM: Homo sapiens

FEATURE:

NAME/KEY: unsure
LOCATION: (4535)
OTHER INFORMATION: n-A,T,C or G
US-09-439-313-536

Query Match 34.6%; Score 21.8; DB 4; Length 6140;
Best Local Similarity 61.4%; Pred. No. 20;
Matches 35; Conservative 0; Mismatches 22; Indels 0; Gaps 0;

QY 6 AAGTACCTTATGCACTTTGTTACTGTTACCGGATGCCGTTCCCAAGCTTTA 62

Db 2405 ACAGTGACATTAGCACTTTGTTGTTGCCAGTATGAAGCCACCAATCTTGA 2349

RESULT 11

US-08-727-118-1/C
Sequence 1, Application US/08727118
Patent No. 5928940

GENERAL INFORMATION:

APPLICANT: MIYAZONO, KOHEI
APPLICANT: SAMPATH, KUBER T.
TITLE OF INVENTION: NOVEL MORPHOGEN-RESPONSIVE SIGNAL
TITLE OF INVENTION: TRANSDUCER AND METHODS OF USE THEREOF
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: CREATIVE BIOMOLECULES, INC.
STREET: 45 SOUTH STREET
CITY: HOPKINTON
STATE: MA
COUNTRY: USA
ZIP: 01748
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/727,118
FILING DATE: 08-OCT-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: VITO PHD, CHRISTINE C.
REGISTRATION NUMBER: 39,061
REFERENCE/DOCKET NUMBER: CRP-121 [2054/91]
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 248-7000
TELEFAX: (617) 248-7100
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 3611 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 905..1264
US-08-727-118-1

Query Match 33.7%; Score 21.2; DB 2; Length 3611;
Best Local Similarity 60.3%; Pred. No. 30;
Matches 35; Conservative 0; Mismatches 23; Indels 0; Gaps 0;

QY 2 GCGGAAGTAACTTATGCACTTTGTTACTGTTACCGGATGCCGTTCCCAAGCT 59

Db 2267 GCAGAGAGAACCTGCTCTTTCTTCATAGAGACCCTGGTCCCGCTCCAAAGTT 2210

RESULT 12
US-08-680-506-4/c
; Sequence 4, Application US/08680506C
; Patent No. 6008013
; GENERAL INFORMATION:

; APPLICANT: Reynolds, Paul R.
; TITLE OF INVENTION: CHONDROCYTE PROTEINS
; FILE REFERENCE: 176/60091
; CURRENT APPLICATION NUMBER: US/08/680,506C
; CURRENT FILING DATE: 1996-07-08
; EARLIER APPLICATION NUMBER: 60/021,672
; EARLIER FILING DATE: 1996-07-05
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 4
; LENGTH: 2233
; TYPE: DNA
; ORGANISM: Gallus gallus
US-08-680-506-4

Query Match 33.0%; Score 20.8; DB 3; Length 2233;
Best Local Similarity 70.0%; Pred. No. 38;
Matches 28; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

OY 9 GTAACTTATGCACTTGTACTGTTACCCGGTATGCCG 48

Db 1708 GTGGCCTCATGCAATTTTATTAGCTTCCAGATGCTG 1669

RESULT 13
US-08-680-506-2/c
; Sequence 2, Application US/08680506C
; Patent No. 6008013
; GENERAL INFORMATION:

; APPLICANT: Reynolds, Paul R.
; TITLE OF INVENTION: CHONDROCYTE PROTEINS
; FILE REFERENCE: 176/60091
; CURRENT APPLICATION NUMBER: US/08/680,506C
; CURRENT FILING DATE: 1996-07-08
; EARLIER APPLICATION NUMBER: 60/021,672
; EARLIER FILING DATE: 1996-07-05
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 2
; LENGTH: 5027
; TYPE: DNA
; ORGANISM: Gallus gallus
US-08-680-506-2

Query Match 33.0%; Score 20.8; DB 3; Length 5027;
Best Local Similarity 70.0%; Pred. No. 46;
Matches 28; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

OY 9 GTAACTTATGCACTTGTACTGTTACCCGGTATGCCG 48

Db 1708 GTGGCCTCATGCAATTTTATTAGCTTCCAGATGCTG 1669

RESULT 14
US-08-680-506-1/c

; Sequence 1, Application US/08680506C
; Patent No. 6008013
; GENERAL INFORMATION:
; APPLICANT: Reynolds, Paul R.
; TITLE OF INVENTION: CHONDROCYTE PROTEINS
; FILE REFERENCE: 176/60091
; CURRENT APPLICATION NUMBER: US/08/680,506C
; CURRENT FILING DATE: 1996-07-08
; EARLIER APPLICATION NUMBER: 60/021,672
; EARLIER FILING DATE: 1996-07-05

; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 1
; LENGTH: 8321
; TYPE: DNA
; ORGANISM: Gallus gallus
US-08-680-506-1

Query Match 33.0%; Score 20.8; DB 3; Length 8321;
Best Local Similarity 70.0%; Pred. No. 52;
Matches 28; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

OY 9 GTAACTTATGCACTTGTACTGTTACCCGGTATGCCG 48

Db 4622 GTGGCCTCATGCAATTTTATTAGCTTCCAGATGCTG 4583

RESULT 15
US-08-181-271A-36/c

; Sequence 36, Application US/08181271A
; Patent No. 5614395
; GENERAL INFORMATION:
; APPLICANT: Ryals, John A.
; APPLICANT: Alexander, Danny C.
; APPLICANT: Beck, James J.
; APPLICANT: Duesing, John H.
; APPLICANT: Friedrich, Leslie B.
; APPLICANT: Goodman, Robert M.
; APPLICANT: Harms, Christian
; APPLICANT: Meins, Jr., Frederick
; APPLICANT: Montoya, Alice
; APPLICANT: Moyer, Mary B.
; APPLICANT: Neuhaus, Jean-Marc
; APPLICANT: Payne, George B.
; APPLICANT: Spertson, Christoph
; APPLICANT: Stinson, Jeffrey R.
; APPLICANT: Ukens, Scott J.
; APPLICANT: Ward, Eric R.
; APPLICANT: Williams, Shericca C.
; TITLE OF INVENTION: CHEMICALLY REGULATABLE AND ANTI-PATHOGENIC
; NUMBER OF SEQUENCES: 106
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CIBA-GEIGY Corporation
; STREET: 7 Skyline Drive
; CITY: Hawthorne
; STATE: New York
; COUNTRY: USA
; ZIP: 10532

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentln Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/181,271A
FILING DATE: 13-JAN-94
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/093,301
FILING DATE: 16-JUL-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/937,197
FILING DATE: 6-NOV-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/678,378
FILING DATE: 1-APR-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/305,566
FILING DATE: 6-FEB-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/165,667
FILING DATE: 8-MAR-1988

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; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/042,847
; FILING DATE: 6-APR-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/632,441
; FILING DATE: 21-DEC-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/425,504
; FILING DATE: 20-OCT-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/848,506
; FILING DATE: 6-MAR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/768,122
; FILING DATE: 27-SEP-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/580,431
; FILING DATE: 7-SEP-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/368,672
; FILING DATE: 20-JUN-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/329,018
; FILING DATE: 24-MAR-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/045,957
; FILING DATE: 12-APR-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Elmer, James Scott
; REGISTRATION NUMBER: 36,129
; REFERENCE/DOCKET NUMBER: S-19825/PL/CGC 1727
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (919)541-8614
; TELEFAX: (919)541-8689
; INFORMATION FOR SEQ ID NO: 36:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12124 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; ORIGINAL SOURCE:
; ORGANISM: Cucumis sativus
; INDIVIDUAL ISOLATE: Cucumber Chitinase Genomic DNA
; IMMEDIATE SOURCE:
; CLONE: pBScucchrht5
; US-08-181-271A-36

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Query Match 33.0%; Score 20.8; DB 1; Length 12124;
Best Local Similarity 70.0%; Fred. No. 37;
Matches 28; Conservative 0; Mismatches 12; Indels 0; Gaps 0;
QY 23 TTGTAACCTGTACCGGTATCCGGTTCACCAAGCTTTA 62
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DB 8248 TTGGAACCTGTGACGCGGCTCCGTTGAGAAAGCTGTA 8209

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 Job time : 32.0806 secs

GenCore version 5.1.4.p5.4578
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OM nucleic - nucleic search, using sw model

Run on: May 24, 2003, 13:48:31 ; Search time 49.1129 Seconds

(without alignments)
1693.834 Million cell updates/sec

Title: US-09-963-803-11

Perfect score: 63

Sequence: 1 ggcggaagtaacctatgc.....tgccggttcccaacttat 63

Scoring table: IDENTITY_NNC

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Searched: 828747 seqs, 660231138 residues

Total number of hits satisfying chosen parameters: 1657494

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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13: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

14: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	63	100.0	63	US-09-963-803-11	Sequence 11, Appl
2	63	100.0	317	US-09-963-803-3	Sequence 3, Appl
3	63	100.0	371	US-09-963-803-5	Sequence 5, Appl
4	61.4	97.5	301	US-09-963-803-7	Sequence 7, Appl
5	61.4	97.5	348	US-09-963-803-4	Sequence 4, Appl
6	61.4	97.5	398	US-09-963-803-6	Sequence 6, Appl
7	42	66.7	243	US-09-963-803-1	Sequence 1, Appl
8	41.2	65.4	392	US-09-963-803-21	Sequence 21, Appl
9	38.8	61.6	604	US-09-963-803-23	Sequence 23, Appl
10	37	58.7	472	US-09-963-803-25	Sequence 25, Appl
11	37	58.7	541	US-09-963-803-24	Sequence 24, Appl
12	35.4	56.2	393	US-09-963-803-19	Sequence 19, Appl
13	35.4	56.2	462	US-09-963-803-20	Sequence 20, Appl
14	35.4	56.2	600	US-09-963-803-22	Sequence 22, Appl
15	24.8	39.4	434	US-09-867-701-2913	Sequence 2913, Ap
16	24.8	39.4	539	US-09-736-457-148	Sequence 148, App
17	24.8	39.4	539	US-09-902-941-148	Sequence 148, App
18	24.8	39.4	539	US-09-849-626-148	Sequence 148, App
19	24.8	39.4	539	US-10-017-754-148	Sequence 148, App

c	20	23.2	36.8	2241	9	US-09-938-842A-646	Sequence 646, App
c	21	22.6	35.9	424	10	US-09-983-965-762	Sequence 762, App
c	22	22.4	35.6	347	10	US-09-867-701-5603	Sequence 5603, App
c	23	22.4	35.6	12010	10	US-09-880-107-3369	Sequence 3369, App
c	24	22.4	35.6	83450	9	US-09-811-469-3	Sequence 3, Appl
c	25	22.2	35.2	771	10	US-09-974-300-2855	Sequence 2855, App
c	26	22.2	35.2	1563	10	US-09-765-705-21	Sequence 21, Appl
c	27	22.2	35.2	2438	9	US-09-822-846-227	Sequence 227, App
c	28	22.2	35.2	684973	10	US-09-263-959-1	Sequence 1, Appl
c	29	22	34.9	1936	10	US-09-833-811-293	Sequence 293, App
c	30	22	34.9	1936	10	US-09-880-107-3832	Sequence 3832, App
c	31	22	34.9	6558	10	US-09-764-877-3503	Sequence 3503, App
c	32	21.8	34.6	1427	10	US-09-925-300-613	Sequence 613, App
c	33	21.8	34.6	3786	9	US-10-012-896-1006	Sequence 1006, App
c	34	21.8	34.6	4395	9	US-10-012-896-1007	Sequence 1007, App
c	35	21.8	34.6	6082	9	US-10-012-896-535	Sequence 535, App
c	36	21.8	34.6	6082	9	US-09-895-793-535	Sequence 535, App
c	37	21.8	34.6	6082	9	US-09-895-814-535	Sequence 535, App
c	38	21.8	34.6	6082	9	US-10-010-940-535	Sequence 535, App
c	39	21.8	34.6	6082	10	US-09-759-143-535	Sequence 535, App
c	40	21.8	34.6	6082	10	US-09-780-669-535	Sequence 535, App
c	41	21.8	34.6	6082	10	US-09-822-827-535	Sequence 535, App
c	42	21.8	34.6	6140	9	US-10-012-896-536	Sequence 536, App
c	43	21.8	34.6	6140	9	US-09-895-793-536	Sequence 536, App
c	44	21.8	34.6	6140	9	US-09-895-814-536	Sequence 536, App
c	45	21.8	34.6	6140	9	US-10-010-940-536	Sequence 536, App

ALIGNMENTS

RESULT 1

US-09-963-803-11

Sequence 11, Application US/09963803

Publication No. US20030028922A1

GENERAL INFORMATION:

APPLICANT: Meristem Therapeutics

TITLE OF INVENTION: Chimeric expression promoters originating from commelina yello

FILE REFERENCE: 184332042

CURRENT APPLICATION NUMBER: US/09/963, 803

CURRENT FILING DATE: 2001-09-26

PRIOR APPLICATION NUMBER: FR 99/03925

PRIOR FILING DATE: 1999-03-29

PRIOR APPLICATION NUMBER: PCT IB00/00370

NUMBER OF SEQ ID NOS: 39

SOFTWARE: PatentIn version 3.1

SEQ ID NO 11

LENGTH: 63

TYPE: DNA

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: S4

US-09-963-803-11

Query Match

Best Local Similarity 100.0%: Score 63; DB 9; Length 63;

Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Query

1 GCGGAAGTAACCTTATGCACTTTTGAACCTGCTACCGGATGCCGTTCCCAAGCTT 60

DB

1 GCGGAAGTAACCTTATGCACTTTTGAACCTGCTACCGGATGCCGTTCCCAAGCTT 60

QY

61 TAT 63

DB

61 TAT 63

RESULT 2

US-09-963-803-3

Sequence 3, Application US/09963803

Publication No. US20030028922A1
GENERAL INFORMATION:
APPLICANT: Meristem Therapeutics
TITLE OF INVENTION: Chimeric expression promoters originating from commelina yellow
FILE REFERENCE: 184332042
CURRENT APPLICATION NUMBER: US/09/963,803
CURRENT FILING DATE: 2001-09-26
PRIOR APPLICATION NUMBER: FR 99/03925
PRIOR FILING DATE: 1999-03-29
PRIOR APPLICATION NUMBER: PCT IB00/00370
PRIOR FILING DATE: 2000-10-05
NUMBER OF SEQ ID NOS: 39
SOFTWARE: PatentIn version 3.1
SEQ ID NO 3
LENGTH: 317
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Promoter MPr1116
NAME/KEY: promoter
LOCATION: (1)..(317)
OTHER INFORMATION:
US-09-963-803-3

Query Match 100.0%; Score 63; DB 9; Length 317;
Best Local Similarity 100.0%; Pred. No. 1.9e-15;

Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCGGGAAGTAACCTTATGATTGTGAACCTGTTACCGCGTATGCCGTTCCCAAGCTT 60
DB 195 GCGGGAAGTAACCTTATGATTGTGAACCTGTTACCGCGTATGCCGTTCCCAAGCTT 254

QY 61 TAT 63
DB 255 TAT 257

RESULT 3
US-09-963-803-5

Sequence 5, Application US/09963803
Publication No. US20030028922A1
GENERAL INFORMATION:
APPLICANT: Meristem Therapeutics
TITLE OF INVENTION: Chimeric expression promoters originating from commelina yellow
FILE REFERENCE: 184332042
CURRENT APPLICATION NUMBER: US/09/963,803
CURRENT FILING DATE: 2001-09-26
PRIOR APPLICATION NUMBER: FR 99/03925
PRIOR FILING DATE: 1999-03-29
PRIOR APPLICATION NUMBER: PCT IB00/00370
PRIOR FILING DATE: 2000-10-05
NUMBER OF SEQ ID NOS: 39
SOFTWARE: PatentIn version 3.1
SEQ ID NO 5
LENGTH: 371
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Promoter MPr1146
NAME/KEY: promoter
LOCATION: (1)..(371)
OTHER INFORMATION:
US-09-963-803-5

Query Match 100.0%; Score 63; DB 9; Length 371;
Best Local Similarity 100.0%; Pred. No. 2e-15;

Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCGGGAAGTAACCTTATGATTGTGAACCTGTTACCGCGTATGCCGTTCCCAAGCTT 60

DB 249 GCGGGAAGTAACCTTATGATTGTGAACCTGTTACCGCGTATGCCGTTCCCAAGCTT 308
QY 61 TAT 63
DB 309 TAT 311

RESULT 4
US-09-963-803-7

Sequence 7, Application US/09963803
Publication No. US20030028922A1
GENERAL INFORMATION:
APPLICANT: Meristem Therapeutics
TITLE OF INVENTION: Chimeric expression promoters originating from commelina yellow
FILE REFERENCE: 184332042
CURRENT APPLICATION NUMBER: US/09/963,803
CURRENT FILING DATE: 2001-09-26
PRIOR APPLICATION NUMBER: FR 99/03925
PRIOR FILING DATE: 1999-03-29
PRIOR APPLICATION NUMBER: PCT IB00/00370
PRIOR FILING DATE: 2000-10-05
NUMBER OF SEQ ID NOS: 39
SOFTWARE: PatentIn version 3.1
SEQ ID NO 7
LENGTH: 301
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Promoter MPr1154
NAME/KEY: promoter
LOCATION: (1)..(301)
OTHER INFORMATION:
US-09-963-803-7

Query Match 97.5%; Score 61.4; DB 9; Length 301;
Best Local Similarity 98.4%; Pred. No. 8.1e-15;

Matches 62; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GCGGGAAGTAACCTTATGATTGTGAACCTGTTACCGCGTATGCCGTTCCCAAGCTT 60
DB 181 GCGGGAAGTAACCTTATGATTGTGAACCTGTTACCGCGTATGCCGTTCCCAAGCTT 240

QY 61 TAT 63
DB 241 TAT 243

RESULT 5
US-09-963-803-4

Sequence 4, Application US/09963803
Publication No. US20030028922A1
GENERAL INFORMATION:
APPLICANT: Meristem Therapeutics
TITLE OF INVENTION: Chimeric expression promoters originating from commelina yellow
FILE REFERENCE: 184332042
CURRENT APPLICATION NUMBER: US/09/963,803
CURRENT FILING DATE: 2001-09-26
PRIOR APPLICATION NUMBER: FR 99/03925
PRIOR FILING DATE: 1999-03-29
PRIOR APPLICATION NUMBER: PCT IB00/00370
PRIOR FILING DATE: 2000-10-05
NUMBER OF SEQ ID NOS: 39
SOFTWARE: PatentIn version 3.1
SEQ ID NO 4
LENGTH: 348
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Promoter MPr1117

Query Match 100.0%; Score 63; DB 9; Length 348;
Best Local Similarity 100.0%; Pred. No. 2e-15;

Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCGGGAAGTAACCTTATGATTGTGAACCTGTTACCGCGTATGCCGTTCCCAAGCTT 60

FEATURE:
NAME/KEY: Promoter
LOCATION: (1)..(348)
OTHER INFORMATION:
US-09-963-803-4

Query Match
Best Local Similarity 97.5%; Score 61.4; DB 9; Length 348;
Pred. No. 8.5e-15;
Matches 62; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GCGGGAAGTACCTTATGCTTGTGTAACCTGTTACCCGGTATCCGGTCCCAAGCTT 60
|||||
DB 228 GCGGGAAGTACCTTATGCTTGTGTAACCTGTTACCCGGTATCCGGTCCCAAGCTT 287

QY 61 TAT 63
|||
DB 288 TAT 290

RESULT 6
US-09-963-803-6

Sequence 6, Application US/09963803
Publication No. US20030028922A1

GENERAL INFORMATION:

APPLICANT: Meristem Therapeutics

TITLE OF INVENTION: Chimeric expression promoters originating from commelina yellow

FILE REFERENCE: 184332042

CURRENT APPLICATION NUMBER: US/09/963,803

PRIOR FILING DATE: 2001-09-26

PRIOR APPLICATION NUMBER: FR 99/03925

PRIOR FILING DATE: 1999-03-29

PRIOR APPLICATION NUMBER: PCT IB00/00370

NUMBER OF SEQ ID NOS: 39

SOFTWARE: PatentIn version 3.1

SEQ ID NO 6

LENGTH: 398

TYPE: DNA

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: promoter MPr1147

FEATURE:

NAME/KEY: promoter

LOCATION: (1)..(398)

OTHER INFORMATION:

US-09-963-803-6

Query Match

Best Local Similarity 97.5%; Score 61.4; DB 9; Length 398;
Pred. No. 8.9e-15;
Matches 62; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GCGGGAAGTACCTTATGCTTGTGTAACCTGTTACCCGGTATCCGGTCCCAAGCTT 60
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DB 278 GCGGGAAGTACCTTATGCTTGTGTAACCTGTTACCCGGTATCCGGTCCCAAGCTT 337

QY 61 TAT 63
|||
DB 338 TAT 340

RESULT 7
US-09-963-803-1

Sequence 1, Application US/09963803
Publication No. US20030028922A1

GENERAL INFORMATION:

APPLICANT: Meristem Therapeutics

TITLE OF INVENTION: Chimeric expression promoters originating from commelina yellow

FILE REFERENCE: 184332042

CURRENT APPLICATION NUMBER: US/09/963,803

PRIOR FILING DATE: 2001-09-26

PRIOR APPLICATION NUMBER: FR 99/03925

Query Match

Best Local Similarity 97.5%; Score 61.4; DB 9; Length 398;
Pred. No. 8.9e-15;
Matches 62; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GCGGGAAGTACCTTATGCTTGTGTAACCTGTTACCCGGTATCCGGTCCCAAGCTT 60
|||||
DB 278 GCGGGAAGTACCTTATGCTTGTGTAACCTGTTACCCGGTATCCGGTCCCAAGCTT 337

QY 61 TAT 63
|||
DB 338 TAT 340

PRIOR FILING DATE: 1999-03-29
PRIOR APPLICATION NUMBER: PCT IB00/00370
PRIOR FILING DATE: 2000-10-05
NUMBER OF SEQ ID NOS: 39
SOFTWARE: PatentIn version 3.1
SEQ ID NO 1
LENGTH: 243
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: 243 bp Fragment from the intergenic region of commelina yellow

QY 1 GCGGGAAGTACCTTATGCTTGTGTAACCTGTTACCCGGTATCCGGTCCCAAGCTT 60
|||||
DB 197 GCGGGAAGTACCTTATGCTTGTGTAACCTGTTACCCGGTATCCGGTCCCAAGCTT 256

QY 61 TAT 62
|||
DB 257 TAT 258

RESULT 8
US-09-963-803-21

Sequence 21, Application US/09963803
Publication No. US20030028922A1

GENERAL INFORMATION:

APPLICANT: Meristem Therapeutics

TITLE OF INVENTION: Chimeric expression promoters originating from commelina yellow

FILE REFERENCE: 184332042

CURRENT APPLICATION NUMBER: US/09/963,803

PRIOR FILING DATE: 2001-09-26

PRIOR APPLICATION NUMBER: PCT IB00/00370

NUMBER OF SEQ ID NOS: 39

SOFTWARE: PatentIn version 3.1

SEQ ID NO 21

LENGTH: 392

TYPE: DNA

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: promoter MPr1164

FEATURE:

NAME/KEY: promoter

LOCATION: (1)..(392)

OTHER INFORMATION:

US-09-963-803-21

Query Match

Best Local Similarity 65.4%; Score 41.2; DB 9; Length 392;
Pred. No. 1e-06;
Matches 49; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

QY 1 GCGGGAAGTACCTTATGCTTGTGTAACCTGTTACCCGGTATCCGGTCCCAAGCTT 60
|||||
DB 197 GCGGGAAGTACCTTATGCTTGTGTAACCTGTTACCCGGTATCCGGTCCCAAGCTT 256

QY 61 TAT 62
|||
DB 257 TAT 258

RESULT 9
US-09-963-803-23

Sequence 23, Application US/09963803
Publication No. US20030028922A1

GENERAL INFORMATION:

APPLICANT: Meristem Therapeutics

TITLE OF INVENTION: Chimeric expression promoters originating from commelina yellow

FILE REFERENCE: 184332042

CURRENT APPLICATION NUMBER: US/09/963,803

PRIOR FILING DATE: 2001-09-26

PRIOR APPLICATION NUMBER: FR 99/03925

PRIOR FILING DATE: 1999-03-29

PRIOR APPLICATION NUMBER: PCT IB00/00370

NUMBER OF SEQ ID NOS: 39

SOFTWARE: PatentIn version 3.1

SEQ ID NO 21

LENGTH: 392

TYPE: DNA

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: promoter MPr1164

FEATURE:

NAME/KEY: promoter

LOCATION: (1)..(392)

OTHER INFORMATION:

US-09-963-803-21

Query Match

Best Local Similarity 65.4%; Score 41.2; DB 9; Length 392;
Pred. No. 1e-06;
Matches 49; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

QY 1 GCGGGAAGTACCTTATGCTTGTGTAACCTGTTACCCGGTATCCGGTCCCAAGCTT 60
|||||
DB 197 GCGGGAAGTACCTTATGCTTGTGTAACCTGTTACCCGGTATCCGGTCCCAAGCTT 256

QY 61 TAT 62
|||
DB 257 TAT 258

GENERAL INFORMATION:
APPLICANT: Meristem Therapeutics
TITLE OF INVENTION: Chimeric expression promoters originating from commelina yellow
FILE REFERENCE: 184332042
CURRENT APPLICATION NUMBER: US/09/963,803
PRIORITY FILING DATE: 2001-09-26
PRIORITY FILING DATE: 1999-03-29
PRIORITY FILING DATE: 2000-10-05
NUMBER OF SEQ ID NOS: 39
SOFTWARE: PatentIn version 3.1
SEQ ID NO: 23
LENGTH: 604
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: promoter MPr1167
FEATURE:
NAME/KEY: promoter
LOCATION: (1)..(604)
OTHER INFORMATION:
US-09-963-803-23

Query Match 61.6%; Score 38.8; DB 9; Length 604;
Best Local Similarity 95.2%; Pred. No. 1e-05;
Matches 40; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 GCGGAAAGTAACTTATGATTGTGAACCTGGTAC 42
DB 278 GCGGAAAGTAACTTATGATTGTGAACCTGGTAC 319

RESULT 10
US-09-963-803-25
Sequence 25, Application US/09963803
Publication No. US20030028922A1
GENERAL INFORMATION:
APPLICANT: Meristem Therapeutics
TITLE OF INVENTION: Chimeric expression promoters originating from commelina yellow
FILE REFERENCE: 184332042
CURRENT APPLICATION NUMBER: US/09/963,803
PRIORITY FILING DATE: 2001-09-26
PRIORITY FILING DATE: 1999-03-29
PRIORITY FILING DATE: 2000-10-05
NUMBER OF SEQ ID NOS: 39
SOFTWARE: PatentIn version 3.1
SEQ ID NO: 25
LENGTH: 472
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: promoter MPr1169
FEATURE:
NAME/KEY: promoter
LOCATION: (1)..(472)
OTHER INFORMATION:
US-09-963-803-25

Query Match 58.7%; Score 37; DB 9; Length 472;
Best Local Similarity 100.0%; Pred. No. 5e-05;
Matches 37; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GCGGAAAGTAACTTATGATTGTGAACCTGGTAC 37
DB 278 GCGGAAAGTAACTTATGATTGTGAACCTGGTAC 314

RESULT 11

US-09-963-803-24
Sequence 24, Application US/09963803
Publication No. US20030028922A1
GENERAL INFORMATION:
APPLICANT: Meristem Therapeutics
TITLE OF INVENTION: Chimeric expression promoters originating from commelina yellow
FILE REFERENCE: 184332042
CURRENT APPLICATION NUMBER: US/09/963,803
PRIORITY FILING DATE: 2001-09-26
PRIORITY FILING DATE: 1999-03-29
PRIORITY FILING DATE: 2000-10-05
NUMBER OF SEQ ID NOS: 39
SOFTWARE: PatentIn version 3.1
SEQ ID NO: 24
LENGTH: 541
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: promoter MPr1168
FEATURE:
NAME/KEY: promoter
LOCATION: (1)..(541)
OTHER INFORMATION:
US-09-963-803-24

Query Match 58.7%; Score 37; DB 9; Length 541;
Best Local Similarity 100.0%; Pred. No. 5.2e-05;
Matches 37; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GCGGAAAGTAACTTATGATTGTGAACCTGGTAC 37
DB 278 GCGGAAAGTAACTTATGATTGTGAACCTGGTAC 314

RESULT 12
US-09-963-803-19
Sequence 19, Application US/09963803
Publication No. US20030028922A1
GENERAL INFORMATION:
APPLICANT: Meristem Therapeutics
TITLE OF INVENTION: Chimeric expression promoters originating from commelina yellow
FILE REFERENCE: 184332042
CURRENT APPLICATION NUMBER: US/09/963,803
PRIORITY FILING DATE: 2001-09-26
PRIORITY FILING DATE: 1999-03-29
PRIORITY FILING DATE: 2000-10-05
NUMBER OF SEQ ID NOS: 39
SOFTWARE: PatentIn version 3.1
SEQ ID NO: 19
LENGTH: 393
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: promoter MPr1162
FEATURE:
NAME/KEY: promoter
LOCATION: (1)..(393)
OTHER INFORMATION:
US-09-963-803-19

Query Match 56.2%; Score 35.4; DB 9; Length 393;
Best Local Similarity 97.3%; Pred. No. 0.0002;
Matches 36; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 GCGGAAAGTAACTTATGATTGTGAACCTGGTAC 37
DB 197 GCGGAAAGTAACTTATGATTGTGAACCTGGTAC 233

RESULT 13

US-09-963-803-20
; Sequence 20, Application US/09963803
; Publication No. US20030028922A1
; GENERAL INFORMATION:
; APPLICANT: Meristem Therapeutics
; TITLE OF INVENTION: Chimeric expression promoters originating from commelina yellow
; FILE REFERENCE: 184332042
; CURRENT APPLICATION NUMBER: US/09/963,803
; PRIOR FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: FR 99/03925
; PRIOR FILING DATE: 1999-03-29
; PRIOR APPLICATION NUMBER: PCT IB00/00370
; PRIOR FILING DATE: 2000-10-05
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 20
; LENGTH: 462
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: promoter MP1163
; NAME/KEY: Promoter
; LOCATION: (1)..(462)
; OTHER INFORMATION:
US-09-963-803-20

Query Match

Best Local Similarity 56.2%; Score 35.4; DB 9; Length 462;
Matches 36; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GCGGGAAGTACCTTATGCTTTGTAAGTTGGTTAC 37
DB 197 GCGGGAAGTACCTTATGCTTTGTAAGTTGGTTAC 233

RESULT 14

US-09-963-803-22
; Sequence 22, Application US/09963803
; Publication No. US20030028922A1
; GENERAL INFORMATION:
; APPLICANT: Meristem Therapeutics
; TITLE OF INVENTION: Chimeric expression promoters originating from commelina yellow
; FILE REFERENCE: 184332042
; CURRENT APPLICATION NUMBER: US/09/963,803
; PRIOR FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: FR 99/03925
; PRIOR FILING DATE: 1999-03-29
; PRIOR APPLICATION NUMBER: PCT IB00/00370
; PRIOR FILING DATE: 2000-10-05
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 22
; LENGTH: 600
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: promoter MP1165
; NAME/KEY: Promoter
; LOCATION: (1)..(600)
; OTHER INFORMATION:
US-09-963-803-22

Query Match 56.2%; Score 35.4; DB 9; Length 600;
Best Local Similarity 97.3%; Pred. No. 0.00024;
Matches 36; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GCGGGAAGTACCTTATGCTTTGTAAGTTGGTTAC 37
DB 197 GCGGGAAGTACCTTATGCTTTGTAAGTTGGTTAC 233

RESULT 15

US-09-867-701-2913/c
; Sequence 2913, Application US/09867701
; Patent No. US20020132237A1
; GENERAL INFORMATION:
; APPLICANT: Agiate, Paul A.
; APPLICANT: Harlocker, Susan L.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.497
; CURRENT APPLICATION NUMBER: US/09/867,701
; PRIOR FILING DATE: 2001-05-29
; NUMBER OF SEQ ID NOS: 10912
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2913
; LENGTH: 434
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-867-701-2913

Query Match

Best Local Similarity 39.4%; Score 24.8; DB 10; Length 434;
Matches 38; Conservative 0; Mismatches 22; Indels 0; Gaps 0;

QY 4 GGAAGTACCTTATGCTTTGTAAGTTGGTTACCGGTTCCCAAGCTTAT 63
DB 92 GGAAGTACCTTATGCTTTGTAAGTTGGTTACCGGTTCCCAAGCTTAT 33

Search completed: May 24, 2003, 15:36:01
Job time : 51.1129 secs

GenCore version 5.1.4-p5.4578
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OM nucleic - nucleic search, using sw model

Run on: May 24, 2003, 11:30:46 ; Search time 827.806 Seconds
(without alignments)
1232.553 Million cell updates/sec

Title: US-09-963-803-11

Perfect score: 63

Sequence: 1 ggcggaagtaaccttatgc.....tgcggtcccaaccttat 63

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :
EST:
1: em_estda:
2: em_esthum:
3: em_estin:
4: em_estnu:
5: em_estov:
6: em_estpl:
7: em_estro:
8: em_hic:
9: gb_est1:
10: gb_est2:
11: gb_hic:
12: gb_est3:
13: gb_est4:
14: gb_est5:
15: em_estfun:
16: em_estom:
17: gb_gss:
18: em_gss_hum:
19: em_gss_inv:
20: em_gss_pln:
21: em_gss_vit:
22: em_gss_fun:
23: em_gss_man:
24: em_gss_mus:
25: em_gss_other:
26: em_gss_pro:
27: em_gss_rtd:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Query Length	ID	Description
1	26.8	42.5	501	14	C88100
2	26.4	41.9	501	17	AO155647 HS_3124.A
3	25	39.7	608	17	BH764088 BMBAC321H
4	25	39.7	835	17	BH183804
5	25	39.7	835	17	CNS070W0
6	24.8	39.4	426	14	R54659

C 7	24.8	39.4	434	9	AA291914
C 8	24.8	39.4	493	12	AA290875
C 9	24.8	39.4	519	12	BG150109
C 10	24.8	39.4	554	9	AI970488
C 11	24.8	39.4	730	10	AW965172
C 12	24.8	39.4	811	12	BF107114
C 13	24.8	39.4	918	12	BF970066
C 14	24.6	39.0	487	17	AZ315498
C 15	24.6	39.0	508	17	BH116178
C 16	24.6	39.0	555	17	AA991986
C 17	24.6	39.0	575	10	AW642223
C 18	24.4	38.7	941	17	BF887280
C 19	24.4	38.7	941	17	CNS04Q20
C 20	24.2	38.4	660	17	AL753769
C 21	24.2	38.4	660	17	AZ48475
C 22	24.2	38.4	662	17	BH099091
C 23	24.2	38.4	734	13	BI819991
C 24	24.2	38.1	430	14	C98647
C 25	23.8	37.8	319	10	BB100921
C 26	23.8	37.8	374	9	AL798232
C 27	23.8	37.8	494	12	BF475316
C 28	23.8	37.8	505	17	BH710571
C 29	23.8	37.8	617	17	AZ448984
C 30	23.8	37.8	617	17	AG162422
C 31	23.8	37.8	676	9	AI894134
C 32	23.8	37.8	731	17	AQ840684
C 33	23.8	37.8	756	10	BE566186
C 34	23.8	37.8	994	13	BI827495
C 35	23.8	37.8	1101	17	CNS00ENB
C 36	23.8	37.8	1163	13	BI757922
C 37	23.6	37.5	435	17	AZ433575
C 38	23.6	37.5	435	17	AQ266202
C 39	23.6	37.5	496	9	AA056419
C 40	23.6	37.5	718	17	BB6730
C 41	23.6	37.5	875	17	BH055813
C 42	23.6	37.5	1080	14	BM912940
C 43	23.4	37.1	219	10	BB474709
C 44	23.4	37.1	219	10	BB474710
C 45	23.4	37.1	220	9	AV164020

ALIGNMENTS

RESULT 1
LOCUS C88100 501 bp mRNA linear EST 11-MAR-1998
DEFINITION C88100 Mouse fertilized one-cell embryo cDNA Mus musculus cDNA
ACCESSION C88100
VERSION C88100.1 GI:2920057
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murine; Mus.
REFERENCE 1 (bases 1 to 501)
Ko,M.S.H, Kitchen,J.R., Wang,X., Wang,X., Threast,T.A., Sun,T., Deraina,G.E., Liang,Y., Kargul,G.J., Sharrara,R., Peonessa,P.D. and Doi,H.
Systematic analyses of genes expressed in fertilized mouse eggs (The ERATO/Doi Project at Wayne State University)
Unpublished (1998)
JOURNAL CONTACT: Hirofumi Doi
COMMENT Doi Bioscience Project, ERATO
Japan Science and Technology Corporation (JST)
WBC Marine East 12F, 2-6 Nakase, Mihama-ku, Chiba 261-71, Japan
Email: hdo@bioa.jst.go.jp.
LOCATION/Qualifiers
FEATURES
SOURCE
1. 501
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"

sequence.
BH183804
CT-163904EA

KEYWORDS	GSS.
SOURCE	Schistosoma mansoni.
ORGANISM	Schistosoma mansoni
REFERENCE	Euhartova, Metazoa: Platyhelminthes; Trematoda: Digenea;
AUTHORS	Strigoidida; Schistosomatidae; Schistosomatidae; Schistosoma
TITLE	1 (bases 1 to 835)
JOURNAL	le Paslier, M.-C., Pierce, R.J., Merlin, F., Hirai, H., Wu, W., Williams
MEDLINE	, D.L., Johnston, D., Loverde, P.T. and le Paslier, D.
COMMENT	Construction and characterization of a Schistosoma mansoni
	bacterial artificial chromosome library
	Genomics 65 (2), 87-94 (2000)
	20247247
	Other_GSSs: 024_O-09-rev
	Contact: Pierce RJ
	INSERM U 167
	Institut Pasteur de Lille
	1 rue du professeur A. Calmette, 59019-Lille, France
	Tel: (33) (0)3 20877783
	Fax: (33) (0)3 20877888
	Email: Raymond.Pierce@pasteur-lille.fr
	CNS sequencing ID=D60AA024AH05CPl
	Plate: 024 row: 0 column: 09
	Seq primer: M13 -21 primer
	Class: BAC ends
	High quality sequence stop: 835.
FEATURES	Location/Qualifiers
source	1..835
	/organism="Schistosoma mansoni"
	/strain="puerto-rican"
	/db_xref="taxon:6183"
	/clone="024009"
	/clone_lib="SmbAc1"
	/sex="mixed"
	/dev_stage="cercariae"
	/lab_host="Blompharia glabrata"
	/note="Vector: pBlotBAC 11; Site_1: Hind III; Partially
	Hind III digested and size-selected S. mansoni cercarial
	DNA was ligated into Hind III digested pBlotBAC 11 vector
	and used to transform E. coli DH10B. The complete library
	contains 23808 clones from 4 independent
	sizing-ligation-transformations. Average insert size
	ranges from 70-127 kb and genome coverage is 7.9-fold."
BASE COUNT	273 a 147 c 141 g 261 t 13 others
ORIGIN	
Query Match	39.7%; Score 25; DB 17; Length 835;
Best local Similarity	75.6%; Pred. No. 39;
Matches 31; Conservative 0; Mismatches 10; Indels 0; Gaps 0;	
cy 6 AAGTAACTTATGATTTGACTTGTTGCTTACCCGCTATGC 46	
Db 69 AAGTAACTTATGCTTTCAACCTGATTAACGCGTATTC 109	
LOCUS	CNS070W0 835 bp DNA linear GSS 10-OCT-2001
DEFINITION	T7 end of clone 024AH05 of library SmbAc1 from strain Puerto-Rican
ACCESSION	AL620754
VERSION	AL620754.1 GI:16034896
KEYWORDS	GSS.
SOURCE	Schistosoma mansoni.
ORGANISM	Schistosoma mansoni
REFERENCE	Euhartova, Metazoa: Platyhelminthes; Trematoda: Digenea;
AUTHORS	Strigoidida; Schistosomatidae; Schistosomatidae; Schistosoma
TITLE	1 (bases 1 to 835)
JOURNAL	le Paslier, M.-C., Pierce, R.J., Merlin, F., Hirai, H., Wu, W.,
MEDLINE	Williams, D.L., Johnston, D., Loverde, P.T. and le Paslier, D.
COMMENT	Construction and characterization of a Schistosoma mansoni
	bacterial artificial chromosome library
	Genomics 65 (2), 87-94 (2000)
	20247247
	Other_GSSs: 024_O-09-rev
	Contact: Pierce RJ
	INSERM U 167
	Institut Pasteur de Lille
	1 rue du professeur A. Calmette, 59019-Lille, France
	Tel: (33) (0)3 20877783
	Fax: (33) (0)3 20877888
	Email: Raymond.Pierce@pasteur-lille.fr
	CNS sequencing ID=D60AA024AH05CPl
	Plate: 024 row: 0 column: 09
	Seq primer: M13 -21 primer
	Class: BAC ends
	High quality sequence stop: 835.
FEATURES	Location/Qualifiers
source	1..835
	/organism="Schistosoma mansoni"
	/strain="puerto-rican"
	/db_xref="taxon:6183"
	/clone="024009"
	/clone_lib="SmbAc1"
	/sex="mixed"
	/dev_stage="cercariae"
	/lab_host="Blompharia glabrata"
	/note="Vector: pBlotBAC 11; Site_1: Hind III; Partially
	Hind III digested and size-selected S. mansoni cercarial
	DNA was ligated into Hind III digested pBlotBAC 11 vector
	and used to transform E. coli DH10B. The complete library
	contains 23808 clones from 4 independent
	sizing-ligation-transformations. Average insert size
	ranges from 70-127 kb and genome coverage is 7.9-fold."
BASE COUNT	273 a 147 c 141 g 261 t 13 others
ORIGIN	
Query Match	39.7%; Score 25; DB 17; Length 835;
Best local Similarity	75.6%; Pred. No. 39;
Matches 31; Conservative 0; Mismatches 10; Indels 0; Gaps 0;	
cy 6 AAGTAACTTATGATTTGACTTGTTGCTTACCCGCTATGC 46	
Db 69 AAGTAACTTATGCTTTCAACCTGATTAACGCGTATTC 109	
LOCUS	CNS070W0 835 bp DNA linear GSS 10-OCT-2001
DEFINITION	T7 end of clone 024AH05 of library SmbAc1 from strain Puerto-Rican
ACCESSION	AL620754
VERSION	AL620754.1 GI:16034896
KEYWORDS	GSS.
SOURCE	Schistosoma mansoni.
ORGANISM	Schistosoma mansoni
REFERENCE	Euhartova, Metazoa: Platyhelminthes; Trematoda: Digenea;
AUTHORS	Strigoidida; Schistosomatidae; Schistosomatidae; Schistosoma
TITLE	1 (bases 1 to 835)
JOURNAL	le Paslier, M.-C., Pierce, R.J., Merlin, F., Hirai, H., Wu, W.,
MEDLINE	Williams, D.L., Johnston, D., Loverde, P.T. and le Paslier, D.
COMMENT	Construction and characterization of a Schistosoma mansoni
	bacterial artificial chromosome library
	Genomics 65 (2), 87-94 (2000)
	20247247
	Other_GSSs: 024_O-09-rev
	Contact: Pierce RJ
	INSERM U 167
	Institut Pasteur de Lille
	1 rue du professeur A. Calmette, 59019-Lille, France
	Tel: (33) (0)3 20877783
	Fax: (33) (0)3 20877888
	Email: Raymond.Pierce@pasteur-lille.fr
	CNS sequencing ID=D60AA024AH05CPl
	Plate: 024 row: 0 column: 09
	Seq primer: M13 -21 primer
	Class: BAC ends
	High quality sequence stop: 835.
FEATURES	Location/Qualifiers
source	1..835
	/organism="Schistosoma mansoni"
	/strain="puerto-rican"
	/db_xref="taxon:6183"
	/clone="024009"
	/clone_lib="SmbAc1"
	/sex="mixed"
	/dev_stage="cercariae"
	/lab_host="Blompharia glabrata"
	/note="Vector: pBlotBAC 11; Site_1: Hind III; Partially
	Hind III digested and size-selected S. mansoni cercarial
	DNA was ligated into Hind III digested pBlotBAC 11 vector
	and used to transform E. coli DH10B. The complete library
	contains 23808 clones from 4 independent
	sizing-ligation-transformations. Average insert size
	ranges from 70-127 kb and genome coverage is 7.9-fold."
BASE COUNT	273 a 147 c 141 g 261 t 13 others
ORIGIN	
Query Match	39.7%; Score 25; DB 17; Length 835;
Best local Similarity	75.6%; Pred. No. 39;
Matches 31; Conservative 0; Mismatches 10; Indels 0; Gaps 0;	
cy 6 AAGTAACTTATGATTTGACT	

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PUBMED
REFERENCE 10783255
AUTHORS 2 (bases 1 to 835)
TITLE Genoscope.
JOURNAL Direct Submission
Genoscope.
Submitted (05-OCT-2001) Genoscope - Centre National de Sequencage :
BP 191.91006 Evry cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
Web : www.genoscope.cns.fr)
Partially Hind III digested and size-selected S. mansoni cercarial
DNA was ligated into Hind III digested pBeloBAC 11 vector and used
to transform E. coli DH10B. The complete library contains 23808
clones from 4 independent siting-ligation-transformations. Average
insert size ranges from 70-127 kb and genome coverage is 7.9-fold.
location/Qualifiers
1. .835
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/strain="Puerto-Rican"
/db_xref="taxon:6183"
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BASE COUNT 273 a 147 c 141 g 261 t 13 others
ORIGIN
Query Match 39.7%; Score 25; DB 17; Length 835;
Best Local Similarity 75.6%; Pred. NO. 39;
Matches 31; Conservative 0; Mismatches 10; Indels 0; Gaps 0;
Oy 6 AAGTACCTTATGCTTGTACTTGGTTCACCGGTATGC 46
||||| ||||||| || ||| ||||| |||||
Db 69 AAGTCACTTTATGCTTTTCACCACTGATTCGCTTATTC 109
||||| ||||||| || ||| ||||| |||||
RESULT 6
LOCUS y174d07.r1 Soares breast 2nbhst Homo sapiens cDNA clone
DEFINITION IMAGE:154477 5', mRNA sequence.
ACCESSION R54659 426 bp mRNA linear EST 22-MAY-1995
VERSION R34659
KEYWORDS R54659.1 GI:819051
SOURCE EST.
ORGANISM human.
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 426)
Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman
,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J.,
Rifkin,L., Rohlfing,T., Soares,M., Tan,F., Trevasakis,E., Waterston
,R., Williamson,A., Wohlmann,P. and Wilson,R.
The Mashu-Merck EST project
Unpublished (1995)
Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
Insert Size: 721
High quality sequence stops: 315 Source: IMAGE Consortium, LNL
This clone is available royalty-free through LNL; contact the
IMAGE Consortium (info@image.lnl.gov) for further information.
Insert length: 721 Std Error: 0.00
Seq primer: M13RP1
High quality sequence stop: 315.
location/Qualifiers
1. .426
/organism="Homo sapiens"
/db_xref="GDB:566912"
/db_xref="taxon:9606"
/clone="IMAGE:154477"
/clone_1lb="Soares breast 2nbhst"
/sex="Female"
/dev_stage="adult"
FEATURES
SOURCE
location/Qualifiers
1. .426
/organism="Homo sapiens"
/db_xref="GDB:566912"
/db_xref="taxon:9606"
/clone="IMAGE:154477"
/clone_1lb="Soares breast 2nbhst"
/sex="Female"
/dev_stage="adult"

```

```

BASE COUNT      142 a      67 c      75 g      141 t      1 others
ORIGIN
        /lab.host="DH10B (ampicillin resistant)"
        /note="Organ: breast; Vector: pT73D (Pharmacia) with a
        modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st
        strand cDNA was primed with a Not I - oligo(dT) primer [5'-
        TGTTACCAATCTGCAAGTGGAGCGGCCGCCCTCTTTTTTTTTTTT 3'] ,
        double-stranded cDNA was ligated to Eco RI adaptors
        (Pharmacia), digested with Not I and cloned into the Not I
        and Eco RI sites of a modified pT73 vector (Pharmacia) .
        Library went through one round of normalization to a Cot -
        230. Library constructed by Bento Soares and M.Fatima
        Bonaldo."

```

Query Match	39.48	Score 24, 8	DB 14	Length 426
Best Local Similarity	63.38	Pred. No. 39		
Matches	38	Conservative	0	Mismatches 22
				Indels 0
				Gaps 0

```

0y      4  GGAAAGTACCTTATGCATTTTGTAACTTGGTTACCCGGTATGCCGTTCCCAAGCTTAT 63
      || || || || || || || || || || || || || || || || || || || || ||
db     284  GGTAAGCAACATTGTCATTTGTACTGGGTGTTCTAGATCAAACTTCACAAAGCTTAT 225

```

RESULT 7				
AA291914/c				
LOCUS	434 bp	mRNA	linear	EST 16-MAY-1997
DEFINITION	ztc39g01.1 Soares ovary tumor	NbHOT	Homo	sepiens cDNA clone
	IMAGE:724752	5',	mRNA sequence.	

ACCESSION	AA291914	GI:1939892
VERSION	AA291914.1	
KEYWORDS	EST.	
SOURCE	human.	
ORGANISM	Homo sapiens	

REFERENCE
AUTHORS
Hillier, L., Allen, M., Bowles, L., Dubuque, T., Giesel, G., Jost, S.,
1 (bases 1 to 434)
Mammalia; Eutheria; Primates; Carnivora; Homiidae; Homo.
Eumetazoa; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi

TITLE
JOURNAL
COMMENT

Kucaba, T., Lacy, M., Le, N., Lennon, G., Maria, M., Martin, J., Moore, B.,
Steptoe, M., Tan, F., Theising, B., White, Y., Wylie,
'T', Waterston, R., and Wilson, R.
Mashu-merck EST Project 1997
Unpublished (1997)
Contact: Wilson RK

Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: estewatson.wustl.edu
This clone is available royalty-free through INLIL; contact the
IMAGE Consortium (info@image.lnll.gov) for further information.
Seq primer: -26m13 rev2. Et from Amersham
High quality sequence stop: 338.
Location/Qualifiers
1..454

```

/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_1b="IMAGE:724752"
/clone_1lb="Soares ovary tumor NbHOT"
/sex="Female"
/tissue_type="ovarian tumor"
/lab_host="DH10B (ampicillin resistant)"
/notes="Organ: ovary; Vector: pT73 (Pharmacia) with a
modified polylinker; Site_1: Not I - oligo(dT) primer [5'
TGTCACCAATCTGAAGTGGAGCGCGCGGTTTTTTTTTTTTTTT 3'],
double-stranded cDNA was size selected, ligated to Eco RI
adapters (Pharmacia), digested with Not I and cloned into
the Not I and Eco RI sites of a modified pT73 vector
(Pharmacia). Library constructed by Bento Soares and
M.Fatima Bonaldo."

```

Query Match	39.48	Score	24.8	DB	9	Length	434
Best Local Similarity	63.38	Pred. No.	39				
Matches	38	Conservative	0	Mismatches	22	Indels	0
						Gaps	0

Oy 4 GGAAGTAACTTATGACATTGTGACTGGTTACC GGCGTGCCCAAGCTTAT 63
 | | | | | | | | | | | | | | |
Db 92 GGTAGAACAATGTTCATTGTGTA CTGGGTCTTAGATAA ACCTTCACAGCATAT 33

RESULT 8	AA290875/c	493 bp	mRNA	linear	EST 15-AUG-1997
LOCUS	AA290875				
DEFINITION	zs44dd05.r1 NCI-GCAP_GCB1	Homo sapiens	CDNA	clone IMAGE:700329	5'
ACCESSION	AA290875				
	mRNA sequence.				

ACCESSION	AA290873	
VERSION	AA290875.1	GI:1938769
KEYWORDS	EST,	
SOURCE	human.	

ORGANISM

REFERENCE
1 (bases 1 to 493)
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
1 (bases 1 to 493)

JOURNAL COMMENT
 AUTHORS: NCI-CCGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
 TITLE: National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 Tumor Gene Index
 Unpublished (1997)
 Contact: Robert Strausberg, Ph.D.

Email: cgapds-remail.nln.gov
This clone is available royalty-free through LNL; contact the
IMAGE Consortium (info@image.lnl.gov) for further information
Insert Length: 1138 Std Error: 0.00
Seq primer: -28m13 rev2 ET from Amersham
High quality sequence stop: 435.

FEATURES

source

```

/organism="Homo sapiens"
/db_xref="GDB:5739753"
/db_xref="taxon:9606"
/cdb="IMAGE:700329"
/clone_1lb="NCI_CGAP_GCB1"
/tissue_type="germinal center B cell"
/lab_host="DH10B"
/notes="Vector: pT73D-Pac (Pharmacia) with a modified
polylinker. Site_1: Not I; Site_2: Eco RI; 1st strand cDNA
was prepared from human tonsillar cells enriched for
germinal center B cells by flow sorting (CD20+, IgD-),
provided by Dr. Louis M. Staudt (NCI), Dr. David Allman
(NCI) and Dr. Gerald Marti (CBER). cDNA synthesis was
primed with a Not I - oligo(dT) primer
[5'-TGTTACCAATCTGAGAGGGAGGCGCCCTCATTTTTCCTTTTTC-3'
]. Double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Not I and cloned into the Not I
and Eco RI sites of the modified pT73 vector. Library
went through one round of normalization, and was
constructed by Bento Soares and M. Fatima Bonaldo."

```

Query Match	39.48	Score 24.8	DB 9	Length 493
Best Local Similarity	63.38	Pred. No. 41		
Matches 38	Conservative 0	Mismatches 22	Indels 0	Gaps 0

QY 4 GGAAGTACCTTATGCATTGTGTAACCTGGTTACC CGGTATGCCGGTTC CCAAGCTTAT 63
||| ||| | | | | | | | | | | | | | | |
Dd 323 GGTAAGCAACAATTGTCTATTGTCTACTCGGCGTCTCAGATCAAAACCTTCACAACCTTAT 264

RESULT 9
Bg150109

LOCUS	BG150109	519 bp	mRNA	linear	EST 05-FEB-2001
DEFINITION	nad51g04.x1 NCI CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3407047 3', mRNA sequence.				
ACCESSION	BG150109				

VERSION BGI50109.1 GI:12662139
 EST.
 KEYWORDS human.
 SOURCE
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 519)
 AUTHORS NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
 TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 Tumor Gene Index
 JOURNAL Unpublished (1997)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-remail.nih.gov
 Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
 Emmert-Buck, M.D., Ph.D.
 CDNA Library Preparation: M. Bento Soares, Ph.D.
 CDNA Library Arrayed by: Greg Lennon, Ph.D.
 DNA Sequencing by: Washington University Genome Sequencing Center
 Clone distribution: NCI-CGAP clone distribution information can be
 found through the I.M.A.G.E. Consortium/LINL, send email to:
infoimage.linl.gov
 Seq primer: -40UP from Gibco
 High quality sequence stop: 483.
 Location/Qualifiers
 1. 519
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="IMAGE:3407047"
 /clone_1lb="NCI-CGAP_Lu24"
 /tissue_type="carcinoid"
 /lab_host="DH10B"
 /note="Organ: lung; Vector: pT73D-Pac (Pharmacia) with a
 modified polylinker; Plasmid DNA from the normalized
 library NCI CGAP Lu5 was prepared, and ss circles were
 used as tracer in a subtractive hybridization reaction.
 The driver was PCR-amplified cDNAs from a pool of 5,000
 clones made from the same library (clonoids
 1414920-1417991 and 1520904-1522439). Subtraction by Bento
 Soares and M. Fatima Bonaldo."

BASE COUNT 180 a 106 c 81 g 152 t
 ORIGIN
 Query Match 39.4%; Score 24.8; DB 12; Length 519;
 Best Local Similarity 63.3%; Pred. No. 41;
 Matches 38; Conservative 0; Mismatches 22; Indels 0; Gaps 0;

QY 4 GGAAGTAACTTATGCTTGTACCTGCTACCCGCTATGCCGTTCCCACTTAT 63
 Db 452 GGTAAGCAACATTTGTTGTTGTTCTAGATCAACACTTCAACACTTAT 511

RESULT 10 554 bp mRNA linear EST 08-MAR-2000
 LOCUS AI970488
 DEFINITION wq93605.x1 NCI-CGAP-C66 Homo sapiens CDNA clone IMAGE:2479616 3'
 similar to contains Alu repetitive element; mRNA sequence.
 ACCESSION AI970488
 VERSION AI970488.1 GI:5767314
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 554)
 AUTHORS NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
 TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 Tumor Gene Index
 JOURNAL Unpublished (1997)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-remail.nih.gov
 Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael
 R. Emmert-Buck, M.D., Ph.D.

CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
 Bonaldo, Ph.D.
 CDNA Library Arrayed by: Greg Lennon, Ph.D.
 DNA Sequencing by: Washington University Genome Sequencing Center
 Clone distribution: NCI-CGAP clone distribution information can be
 found through the I.M.A.G.E. Consortium/LINL at:
www-bio.linl.gov/bdrp/image/image.html
 Insert Length: 613 Std Error: 0.00
 Seq primer: -40UP from Gibco
 High quality sequence stop: 457.
 Location/Qualifiers
 1. 554
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="IMAGE:2479616"
 /clone_1lb="NCI-CGAP-C66"
 /tissue_type="pooled gemm cell tumors"
 /lab_host="DH10B"
 /note="Vector: pT73D-Pac (Pharmacia) with a modified
 polylinker; Site 1: Not I; Site 2: Eco RI; Plasmid DNA
 from the normalized library NCI CGAP-C64 was prepared, and
 ss circles were made in vitro. Following HAP purification,
 this DNA was used as tracer in a subtractive hybridization
 reaction. The driver was PCR-amplified cDNAs from a pool
 of 5,000 clones made from the same library (clonoids
 1257096-1258631, 1469064-1470983, and 1475592-1476743).
 Subtraction by Bento Soares and M. Fatima Bonaldo."

BASE COUNT 190 a 111 c 89 g 163 t 1 others
 ORIGIN
 Query Match 39.4%; Score 24.8; DB 9; Length 554;
 Best Local Similarity 63.3%; Pred. No. 42;
 Matches 38; Conservative 0; Mismatches 22; Indels 0; Gaps 0;

QY 4 GGAAGTAACTTATGCTTGTACCTGCTACCCGCTATGCCGTTCCCACTTAT 63
 Db 450 GGTAAGCAACATTTGTTGTTGTTCTAGATCAACACTTCAACACTTAT 509

RESULT 11 730 bp mRNA linear EST 01-JUN-2000
 LOCUS AW965172
 DEFINITION EST377245 MAGE resequences, MAGI Homo sapiens CDNA, mRNA sequence.
 ACCESSION AW965172
 VERSION AW965172.1 GI:8155008
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 730)
 AUTHORS Hegde, P., Ol, R., Abernathy, K., Dharap, S., Gaspar, R., Gay, C., Holt,
 J.E., Saeed, A.I., Sharov, V., Lee, N.H., Yeatman, T.J. and
 Quackenbush, J.
 Assessment of gene expression patterns in a model of colon tumor
 metastasis using a 19,200 element CDNA microarray
 Unpublished (2000)
 JOURNAL Contact: John Quackenbush
 COMMENT The Institute for Genomic Research
 9712 Medical Center Dr., Rockville, MD 20850, USA
 Tel: 301 838 3528
 Fax: 301 838 0208
 Email: johnq@ligr.org
 Plate: 211
 Seq primer: Forward.
 Location/Qualifiers
 1. 730
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone_1lb="MAGE resequences, MAGI"
 /note="Vector: BluescriptSKM"

BASE COUNT 255 a 135 c 112 g 228 t
 ORIGIN

Query Match 39.4%; Score 24.8; DB 10; Length 730;
 Best Local Similarity 63.3%; Pred. No. 46;
 Matches 38; Conservative 0; Mismatches 22; Indels 0; Gaps 0;

4 GGAAGTAACCTTATGATTTGTAACCTTGGTTACCCGGTATGCCGGTTCACCAAGCTTAT 63
 Db 448 GGTAAACCAACATTGTTACTGTTACTGGTGTCTAGATCAACCTTACCAAGCTTAT 507

RESULT 12
 BF107114/c 811 bp mRNA linear EST 19-OCT-2000
 LOCUS 601823675F1 NIH_MGC_79 Homo sapiens cDNA clone IMAGE:4043514 5',
 DEFINITION mRNA sequence.
 ACCESSION BF107114
 VERSION BF107114.1 GI:10889555
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 REFERENCE 1 (bases 1 to 811)
 NIH-MGC http://mhc.ncl.nih.gov/
 National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgabbs-remail.nih.gov
 Tissue Procurement: CLONTECH Laboratories, Inc.
 CDNA Library Preparation: CLONTECH Laboratories, Inc.
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov
 Plate: L10C866 row: e column: 19
 High quality sequence stop: 540.

FEATURES
 source Location/Qualifiers
 1..811
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="IMAGE:4043514"
 /clone_lib="NIH_MGC_79"
 /lab_host="DH10B (T1 phage-resistant)"
 /note="Organ: Placenta; Vector: pDNR-LIB (Clontech);
 Site_1: SfiI (ggcgctcgagc); Site_2: SfiI (ggcgctcgagc)
); 5' and 3' adaptors were used in cloning as follows: 5'
 adaptor sequence: 5'-CACGCCATTATGCC-3' and 3' adaptor
 sequence: 5'-ATTCTAGAGCGCGGACGCGACATG-dT(30)BN-3'
 (where B = A, C, G, or T). Average
 insert size 1.3 kb (range 0.5-4.0 kb). 15/15 colonies
 contained inserts by PCR. This library was enriched for
 full-length clones and was constructed by Clontech
 Laboratories (Palo Alto, CA). Note: this is a NIH_MGC
 library."

BASE COUNT 240 a 159 c 153 g 259 t
 ORIGIN

Query Match 39.4%; Score 24.8; DB 12; Length 811;
 Best Local Similarity 63.3%; Pred. No. 47;
 Matches 38; Conservative 0; Mismatches 22; Indels 0; Gaps 0;

4 GGAAGTAACCTTATGATTTGTAACCTTGGTTACCCGGTATGCCGGTTCACCAAGCTTAT 63
 Db 394 GGTAAACCAACATTGTTACTGTTACTGGTGTCTAGATCAACCTTACCAAGCTATAT 335

RESULT 13
 BE970066/c 918 bp mRNA linear EST 22-JAN-2001
 LOCUS 602272333F1 NIH_MGC_84 Homo sapiens cDNA clone IMAGE:4360233 5',
 DEFINITION mRNA sequence.
 ACCESSION BE970066

VERSION BE970066.1 GI:12337281
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 REFERENCE 1 (bases 1 to 918)
 NIH-MGC http://mhc.ncl.nih.gov/
 National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgabbs-remail.nih.gov
 Tissue Procurement: ATCC
 CDNA Library Preparation: Life Technologies, Inc.
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov
 Plate: L10C001 row: b column: 10
 High quality sequence stop: 690.

FEATURES
 source Location/Qualifiers
 1..918
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="IMAGE:4360233"
 /clone_lib="NIH_MGC_84"
 /tissue_type="adrenal cortex carcinoma, cell line"
 /lab_host="DH10B (phage-resistant)"
 /note="Organ: adrenal gland; Vector: pCMV-SPORT6; Site_1:
 NotI; Site_2: SalI; Cloned unidirectionally; oligo-dT
 primed. Average insert size 1.229 kb. Library enriched for
 full-length clones and constructed by Life Technologies.
 Note: this is a NIH_MGC Library."

BASE COUNT 269 a 171 c 173 g 305 t
 ORIGIN

Query Match 39.4%; Score 24.8; DB 12; Length 918;
 Best Local Similarity 63.3%; Pred. No. 49;
 Matches 38; Conservative 0; Mismatches 22; Indels 0; Gaps 0;

4 GGAAGTAACCTTATGATTTGTAACCTTGGTTACCCGGTATGCCGGTTCACCAAGCTTAT 63
 Db 598 GGTAAACCAACATTGTTACTGTTACTGGTGTCTAGATCAACCTTACCAAGCTATAT 539

RESULT 14
 A2315498/c 487 bp DNA linear GSS 29-SEP-2000
 LOCUS 1M0032D15R Mouse 10kb plasmid UGCLM library Mus musculus genomic
 DEFINITION clone UGCLM0032D15 R. DNA sequence.
 ACCESSION A2315498
 VERSION A2315498.1 GI:10362388
 KEYWORDS GSS.
 SOURCE house mouse.
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 REFERENCE 1 (bases 1 to 487)
 Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamill, C.,
 Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly,
 M., Rose, M., Rose, R., Stokes, R., Tinney, A., von Niederhausern, A.
 and Wright, D., Weiss, R.
 Mouse whole genome scaffolding with paired end reads from 10kb
 plasmid inserts
 Unpublished (2000)
 CONTACT: Robert B. Weiss
 University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT
 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177.

Email: ddunne@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0032 row: D column: 15
Seq primer: CACACACGGAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 487.

BASE COUNT	129 a	105 c	83 g	170 t
ORIGIN				

Query Match	39.08;	Score 24.6;	DB 17;	Length 487;
Best Local Similarity	61.98;	Pred. No. 49;		
Matches 39; Conservative	0;	Mismatches 24;	Indels 0;	Gaps 0;

Qy	61	TAT	63
Db	130	TCT	128

LOCUS	DEFINITION	RPCT-24	223H11.TV	RPCT-24	Mus musculus	genomic clone	RPCT-24	223H11	GSS	19-JUL-2001
BH116178/c	LOCUS	508 bp	DNA	linear						
BH116178	DEFINITION	508 bp	DNA	linear						

REFERENCE
AUTHORS
Zhao, S., Niernan, W., Malek, J., Shatsman, S., Akintret, B., Levins, M.,
Eukaryota; Metazoa: Chordata; Craniata; Vertebrata, Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
1 (bases 1 to 508)

TITLE	COMMENT
Mouse BAC End Sequences from Library RPCI-24	
Unpublished (1999)	
Other GSSs: RPCI-24-223H11.TJ	
Contact: Shaying Zhao	
Department of Eukaryotic Genomics	
The Institute for Genomic Research	
9712 Medical Center Dr., Rockville, MD 20850, USA	

Tel: 301 838 0200
Fax: 301 838 0208
Email: szhaoc@tigr.org
Clones are derived from the mouse BAC library RPCI-24. For BAC library availability, please contact Pieter de Jong (pdejong@mai.cho.org). Clones may be purchased from BACPAC Resources (<http://www.choi.1.org/bacpac/orderingframe.htm>). BAC end sequence: <http://www.tigr.org/tdb/bac-ends/mouse/bac-end-intro.html>
plate: 223 row: H column: 11
Seq primer: T7
Class: BAC ends

BASE COUNT	220 a	77 c	70 g	141 t
ORIGIN				

Query Match	39.0%;	Score 24.6;	DB 17;	Length 508;
Best Local Similarity	70.2%;	Pred. No. 49;		
Matches 33; Conservative	0;	Mismatches 14;	Indels 0;	Gaps 0;

```
Search completed: May 24, 2003, 15:33:24
Job time : 831.806 secs
```


score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

Result	Query
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2	2
3	3
4	4
5	5
6	6
7	7
8	8
9	9
10	10
11	11
12	12
13	13
14	14
15	15
16	16
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18	18
19	19
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61	61
62	62
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65	65
66	66
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5225.021 Million cell updates/sec

Title: US-09-963-803-13

Sequence: 1 catgtctgcactagtgtat.....aaggatgcacgcacccact 63

Scoring table: IDENTITY_NUC

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

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Maximum	DB seq	length:	200000000000

Post-processor: MATHS MATCH 08

Listing first 45 summaries

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41:	em_hbg_others.*

Pred. No. is the number of results predicted by chance to have a

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2	63	100.0	63	6	AX036747	AX036747 Sequence
3	59	93.7	280	6	AX036601	AX036601 Sequence
4	59	93.7	301	6	AX036741	AX036741 Sequence
5	59	93.7	398	6	AX036740	AX036740 Sequence
6	59	93.7	472	6	AX036759	AX036759 Sequence
7	59	93.7	541	6	AX036758	AX036758 Sequence
8	59	93.7	604	6	AX036757	AX036757 Sequence
9	46	73.0	79	6	AX036611	AX036611 Sequence
10	46	73.0	79	6	AX036748	AX036748 Sequence
11	46	73.0	259	6	AX036616	AX036616 Sequence
12	46	73.0	296	6	AX036603	AX036603 Sequence
13	46	73.0	371	6	AX036739	AX036739 Sequence
C 14	45	71.4	392	6	AX036735	AX036735 Sequence
15	45	71.4	463	6	AX036753	AX036753 Sequence
16	45	71.4	492	6	AX036754	AX036754 Sequence
17	45	71.4	600	6	AX036756	AX036756 Sequence
18	45	71.4	9285	6	AX093047	AX093047 Sequence
19	45	71.4	15077	6	AX093052	AX093052 Sequence
20	43.4	68.9	174	8	AF434749	AF434749 Zea mays
21	43.4	68.9	189	8	AF164073	AF164073 Sequence
C 22	43.4	68.9	197	8	AF434747	AF434747 Zea mays
23	43.4	68.9	199	8	AF434746	AF434746 Zea mays
24	43.4	68.9	199	8	AF434748	AF434748 Zea mays
C 25	43.4	68.9	199	8	AF434750	AF434750 Zea mays
26	43.4	68.9	240	6	AX033493	AX033493 Sequence
27	43.4	68.9	309	6	AX044092	AX044092 Sequence
28	43.4	68.9	309	6	AX405116	AX405116 Sequence
29	43.4	68.9	331	6	BD001990	BD001990 A transgene
30	43.4	68.9	332	6	BD1311	BD1311 Cauliflower
31	43.4	68.9	333	6	104847	104847 Sequence 3
32	43.4	68.9	354	12	ARCAMVPR	XJ04879 Camv promotr
C 33	43.4	68.9	350	12	SC0380514	SC0380514 Synthetic
34	43.4	68.9	439	6	AA1016	AA1016 Sequence 3
35	43.4	68.9	439	6	AR082579	AR082579 Sequence
36	43.4	68.9	439	6	I28254	I28254 Sequence 3
37	43.4	68.9	446	6	A78762	A78762 Sequence 23
38	43.4	68.9	446	6	AR014735	AR014735 Sequence
39	43.4	68.9	470	6	AX026717	AX026717 Sequence
40	43.4	68.9	480	12	SYNCAMVCM5	M74305 Synthetic e
41	43.4	68.9	522	6	AX405123	AX405123 Sequence
42	43.4	68.9	532	6	AR110594	AR110594 Sequence
43	43.4	68.9	532	6	AR150993	AR150993 Sequence
44	43.4	68.9	532	6	AR152416	AR152416 Sequence
45	43.4	68.9	532	6	AR152425	AR152425 Sequence

ALIGNMENTS

RESULT 1			
AX036610			
LOCUS	AX036610	63 bp	DNA
DEFINITION	Sequence 16 from Patent FR2791358.		linear
			PAT 16-NOV-2000

SOURCE

ORGANISM	synthetic construct	artificial sequences.
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REFERENCE 1 (bases 1 to 63)

AUTHORS Rance, I., Theisen, M. and Gruber, V.
JOURNAL Patent: FR 2791358-A 16 29-SEP-2000;

FEATURES

Location/Qualifiers

```

source
1. .63
/organism="synthetic construct"
/db_xref="taxon:32630"
/note="directional building block S6-directional building
block oligonucleotide for the construction of promoters by
1b-PCR"
BASE COUNT      16 a      14 c      17 g      16 t
ORIGIN
Query Match      100.0%; Score 63; DB 6; Length 63;
Best Local Similarity 100.0%; Pred. No. 1.1e-13;
Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CATGCTGCACAGTATGATGTGATATCTCCACTGACGTAAAGGATGACGATGCC 60
    |||||||
Db 1 CATGCTGCACAGTATGATGTGATATCTCCACTGACGTAAAGGATGACGATGCC 60

OY 61 ACT 63
    |||
Db 61 ACT 63

RESULT 2
AX036747
LOCUS      AX036747      63 bp      DNA      linear      PAT 16-NOV-2000
DEFINITION Sequence 13 from Patent WO0058485.
ACCESSION  AX036747
VERSION     AX036747.1 GI:11226256
KEYWORDS
SOURCE      synthetic construct.
ORGANISM    artificial sequences.
REFERENCE    1 (bases 1 to 63)
AUTHORS      Range,I., Theisen,M. and Gruber,V.
TITLE        Chimeric expression promoters originating from commelina yellow
              mottle virus and cassava vein mosaic virus
              Patent: WO 0058485-A 13 05-OCT-2000;
              MERISTEM THERAPEUTICS (FR) ; RANCE IANN (FR) ; THEISEN MANFRED (FR)
              ; GRUBER VERONIQUE (FR)
FEATURES
source      1. .63
              Location/Qualifiers
              /organism="synthetic construct"
              /db_xref="taxon:32630"
              /note="Directional desoxynucleotide building block S6"
BASE COUNT      16 a      14 c      17 g      16 t
ORIGIN
Query Match      100.0%; Score 63; DB 6; Length 63;
Best Local Similarity 100.0%; Pred. No. 1.1e-13;
Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CATGCTGCACAGTATGATGTGATATCTCCACTGACGTAAAGGATGACGATGCC 60
    |||||||
Db 1 CATGCTGCACAGTATGATGTGATATCTCCACTGACGTAAAGGATGACGATGCC 60

OY 61 ACT 63
    |||
Db 61 ACT 63

RESULT 3
AX036601
LOCUS      AX036601      280 bp      DNA      linear      PAT 16-NOV-2000
DEFINITION Sequence 7 from Patent FR2791358.
ACCESSION  AX036601
VERSION     AX036601.1 GI:11226196
KEYWORDS
SOURCE      synthetic construct.
ORGANISM    artificial sequences.
REFERENCE    1 (bases 1 to 280)
AUTHORS      Range,I., Theisen,M. and Gruber,V.
TITLE        Chimeric expression promoters originating from commelina yellow
              mottle virus and cassava vein mosaic virus
              Patent: FR 2791358-A 7 29-SEP-2000;

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MERISTEM THERAPEUTICS (FR)
Location/Qualifiers
1. .280
/organism="synthetic construct"
/db_xref="taxon:32630"
promoter
1. .280
/note="The promoter Mp1110 was created by inserting at
position -99 bp of Mp1098 an element of 18 bp containing
a 'G' box and by fusing a sequence of 44 bp of the RNA 35S
CAMV promoter
promoter Mp1110"
BASE COUNT      88 a      73 c      42 g      77 t
ORIGIN
Query Match      93.7%; Score 59; DB 6; Length 280;
Best Local Similarity 100.0%; Pred. No. 3.9e-12;
Matches 59; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 CTGCAGACTAGTGTGATGTGATATCTCCACTGACGTAAAGGATGACGATGCCACT 63
    |||||||
Db 13 CTGCAGACTAGTGTGATGTGATATCTCCACTGACGTAAAGGATGACGATGCCACT 71

RESULT 4
AX036741
LOCUS      AX036741      301 bp      DNA      linear      PAT 16-NOV-2000
DEFINITION Sequence 7 from Patent WO0058485.
ACCESSION  AX036741
VERSION     AX036741.1 GI:11226250
KEYWORDS
SOURCE      synthetic construct.
ORGANISM    artificial sequences.
REFERENCE    1 (bases 1 to 301)
AUTHORS      Range,I., Theisen,M. and Gruber,V.
TITLE        Chimeric expression promoters originating from commelina yellow
              mottle virus and cassava vein mosaic virus
              Patent: WO 0058485-A 7 05-OCT-2000;
              MERISTEM THERAPEUTICS (FR) ; RANCE IANN (FR) ; THEISEN MANFRED (FR)
              ; GRUBER VERONIQUE (FR)
FEATURES
source      1. .301
              Location/Qualifiers
              /organism="synthetic construct"
              /db_xref="taxon:32630"
              /note="promoter Mp1154"
BASE COUNT      98 a      54 c      74 g      75 t
ORIGIN
Query Match      93.7%; Score 59; DB 6; Length 301;
Best Local Similarity 100.0%; Pred. No. 3.8e-12;
Matches 59; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 CTGCAGACTAGTGTGATGTGATATCTCCACTGACGTAAAGGATGACGATGCCACT 63
    |||||||
Db 13 CTGCAGACTAGTGTGATGTGATATCTCCACTGACGTAAAGGATGACGATGCCACT 71

RESULT 5
AX036740
LOCUS      AX036740      398 bp      DNA      linear      PAT 16-NOV-2000
DEFINITION Sequence 6 from Patent WO0058485.
ACCESSION  AX036740
VERSION     AX036740.1 GI:11226249
KEYWORDS
SOURCE      synthetic construct.
ORGANISM    artificial sequences.
REFERENCE    1 (bases 1 to 398)
AUTHORS      Range,I., Theisen,M. and Gruber,V.
TITLE        Chimeric expression promoters originating from commelina yellow
              mottle virus and cassava vein mosaic virus
              Patent: WO 0058485-A 6 05-OCT-2000;

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MERISTEM THERAPEUTICS (FR) ; RANCE IANN (FR) ; THEISEN MANFRED (FR)
; GRUBER VERONIQUE (FR)
LOCATION/Qualifiers
source
1. .398
/organism="synthetic construct"
/db_xref="taxon:32630"
/note="Promoter MPr1147"
promoter
1. .398
BASE COUNT 128 a 80 c 93 g 97 t
ORIGIN
Query Match 93.7%; Score 59; DB 6; Length 398;
Best Local Similarity 100.0%; Pred. No. 3.8e-12;
Matches 59; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 5 CTGCAGACTAGTGGATTGATGATATCTCCACGTAGAGGATGAGCGCATGCCACT 63
DB 110 CTGCAGACTAGTGGATTGATGATATCTCCACGTAGAGGATGAGCGCATGCCACT 168
RESULT 6
AX036759 472 bp DNA linear PAT 16-NOV-2000
LOCUS AX036759
DEFINITION Sequence 25 from Patent W00058485.
ACCESSION AX036759
VERSION AX036759.1 GI:11226268
KEYWORDS
SOURCE
synthetic construct.
ORGANISM
artificial sequences.
REFERENCE
1 (bases 1 to 472)
AUTHORS Rance,I., Theisen,M. and Gruber,V.
TITLE Chimeric expression promoters originating from commelina yellow
mottle virus and cassava vein mosaic virus
JOURNAL Patent: WO 0058485-A 25 05-OCT-2000;
MERISTEM THERAPEUTICS (FR) ; RANCE IANN (FR) ; THEISEN MANFRED (FR)
; GRUBER VERONIQUE (FR)
FEATURES
source
1. .472
Location/Qualifiers
/organism="synthetic construct"
/db_xref="taxon:32630"
/note="Promoter MPr1169"
promoter
1. .472
BASE COUNT 149 a 92 c 112 g 119 t
ORIGIN
Query Match 93.7%; Score 59; DB 6; Length 472;
Best Local Similarity 100.0%; Pred. No. 3.8e-12;
Matches 59; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 5 CTGCAGACTAGTGGATTGATGATATCTCCACGTAGAGGATGAGCGCATGCCACT 63
DB 110 CTGCAGACTAGTGGATTGATGATATCTCCACGTAGAGGATGAGCGCATGCCACT 168
RESULT 7
AX036758 541 bp DNA linear PAT 16-NOV-2000
LOCUS AX036758
DEFINITION Sequence 24 from Patent W00058485.
ACCESSION AX036758
VERSION AX036758.1 GI:11226267
KEYWORDS
SOURCE
synthetic construct.
ORGANISM
artificial sequences.
REFERENCE
1 (bases 1 to 541)
AUTHORS Rance,I., Theisen,M. and Gruber,V.
TITLE Chimeric expression promoters originating from commelina yellow
mottle virus and cassava vein mosaic virus
JOURNAL Patent: WO 0058485-A 24 05-OCT-2000;
MERISTEM THERAPEUTICS (FR) ; RANCE IANN (FR) ; THEISEN MANFRED (FR)
; GRUBER VERONIQUE (FR)
FEATURES
source
Location/Qualifiers

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1. .541
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/db_xref="taxon:32630"
/note="Promoter MPr1168"
promoter
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BASE COUNT 169 a 104 c 130 g 138 t
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Query Match 93.7%; Score 59; DB 6; Length 541;
Best Local Similarity 100.0%; Pred. No. 3.7e-12;
Matches 59; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 5 CTGCAGACTAGTGGATTGATGATATCTCCACGTAGAGGATGAGCGCATGCCACT 63
DB 110 CTGCAGACTAGTGGATTGATGATATCTCCACGTAGAGGATGAGCGCATGCCACT 168
RESULT 8
AX036757 604 bp DNA linear PAT 16-NOV-2000
LOCUS AX036757
DEFINITION Sequence 23 from Patent W00058485.
ACCESSION AX036757
VERSION AX036757.1 GI:11226266
KEYWORDS
SOURCE
synthetic construct.
ORGANISM
artificial sequences.
REFERENCE
1 (bases 1 to 604)
AUTHORS Rance,I., Theisen,M. and Gruber,V.
TITLE Chimeric expression promoters originating from commelina yellow
mottle virus and cassava vein mosaic virus
JOURNAL Patent: WO 0058485-A 23 05-OCT-2000;
MERISTEM THERAPEUTICS (FR) ; RANCE IANN (FR) ; THEISEN MANFRED (FR)
; GRUBER VERONIQUE (FR)
FEATURES
source
1. .604
Location/Qualifiers
/organism="synthetic construct"
/db_xref="taxon:32630"
/note="Promoter MPr1167"
promoter
1. .604
BASE COUNT 186 a 116 c 145 g 157 t
ORIGIN
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Best Local Similarity 100.0%; Pred. No. 3.7e-12;
Matches 59; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 5 CTGCAGACTAGTGGATTGATGATATCTCCACGTAGAGGATGAGCGCATGCCACT 63
DB 110 CTGCAGACTAGTGGATTGATGATATCTCCACGTAGAGGATGAGCGCATGCCACT 168
RESULT 9
AX036611 79 bp DNA linear PAT 16-NOV-2000
LOCUS AX036611
DEFINITION Sequence 17 from Patent FR2791358.
ACCESSION AX036611
VERSION AX036611.1 GI:11226206
KEYWORDS
SOURCE
synthetic construct.
ORGANISM
artificial sequences.
REFERENCE
1 (bases 1 to 79)
AUTHORS Rance,I., Theisen,M. and Gruber,V.
TITLE Chimeric expression promoters originating from commelina yellow
mottle virus and cassava vein mosaic virus
JOURNAL Patent: FR 2791358-A 17 29-SEP-2000;
MERISTEM THERAPEUTICS (FR)
FEATURES
source
Location/Qualifiers
/organism="synthetic construct"
/db_xref="taxon:32630"
/note="directional building block S7-directional building
block oligonucleotide for the construction of promoters by
1b-PCR"

BASE COUNT 22 a 15 c 20 g 22 t
ORIGIN

Query Match 73.0%; Score 46; DB 6; Length 79;
Best Local Similarity 100.0%; Pred. No. 5.1e-07;
Matches 46; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 18 GATTGATGATATCTCCACTGACGTAAAGGATGACGATGCCACT 63
Db 34 GATTGATGATATCTCCACTGACGTAAAGGATGACGATGCCACT 79

RESULT 10
LOCUS AX036748 79 bp DNA linear PAT 16-NOV-2000
DEFINITION Sequence 14 from Patent WO0058485.
ACCESSION AX036748
VERSION AX036748.1 GI:11226257
KEYWORDS
SOURCE
ORGANISM
synthetic construct.
artificial sequences.
REFERENCE 1 (bases 1 to 79)
AUTHORS Rance, I., Theisen, M. and Gruber, V.
TITLE Chimeric expression promoters originating from commelina yellow
mottle virus and cassava vein mosaic virus
PATENT: WO 0058485-A 14 05-OCT-2000;
JOURNAL MERISTEM THERAPEUTICS (FR) ; RANCE IANN (FR) ; THEISEN MANFRED (FR)
FEATURES
source
1. .79
/organism="synthetic construct"
/db_xref="taxon:32630"
/note="directional desoxynucleotide building block 87"

BASE COUNT 22 a 15 c 20 g 22 t
ORIGIN

Query Match 73.0%; Score 46; DB 6; Length 79;
Best Local Similarity 100.0%; Pred. No. 5.1e-07;
Matches 46; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 18 GATTGATGATATCTCCACTGACGTAAAGGATGACGATGCCACT 63
Db 34 GATTGATGATATCTCCACTGACGTAAAGGATGACGATGCCACT 79

RESULT 11
LOCUS AX036616 259 bp DNA linear PAT 16-NOV-2000
DEFINITION Sequence 22 from Patent FR2791358.
ACCESSION AX036616
VERSION AX036616.1 GI:11226211
KEYWORDS
SOURCE
ORGANISM
synthetic construct.
artificial sequences.
REFERENCE 1 (bases 1 to 259)
AUTHORS Rance, I., Theisen, M. and Gruber, V.
TITLE Chimeric expression promoters originating from commelina yellow
mottle virus and cassava vein mosaic virus
PATENT: FR 2791358-A 22 29-SEP-2000;
JOURNAL MERISTEM THERAPEUTICS (FR)
FEATURES
source
1. .259
/organism="synthetic construct"
/db_xref="taxon:32630"
/note="Promoter MPr1112 differs from MPr1111 by a deletion
of 35 bp containing the 'G' box and stretching from
position -127 to position -89 and a deletion of two bp
situated at positions -78 and -76
promoter MPr1112"

BASE COUNT 82 a 67 c 38 g 72 t
ORIGIN

Query Match 73.0%; Score 46; DB 6; Length 259;
Best Local Similarity 100.0%; Pred. No. 4.8e-07;
Matches 46; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 18 GATTGATGATATCTCCACTGACGTAAAGGATGACGATGCCACT 63
Db 42 GATTGATGATATCTCCACTGACGTAAAGGATGACGATGCCACT 87

RESULT 12
LOCUS AX036603 296 bp DNA linear PAT 16-NOV-2000
DEFINITION Sequence 9 from Patent FR2791358.
ACCESSION AX036603
VERSION AX036603.1 GI:11226198
KEYWORDS
SOURCE
ORGANISM
synthetic construct.
artificial sequences.
REFERENCE 1 (bases 1 to 296)
AUTHORS Rance, I., Theisen, M. and Gruber, V.
TITLE Chimeric expression promoters originating from commelina yellow
mottle virus and cassava vein mosaic virus
PATENT: FR 2791358-A 9 29-SEP-2000;
JOURNAL MERISTEM THERAPEUTICS (FR)
FEATURES
source
1. .296
/organism="synthetic construct"
/db_xref="taxon:32630"
/note="Promoter MPr1111 created by inserting at -99 bp
position of MPr1098, an 18 bp element containing a 'G' box
and fusing a sequence of 58 bp (duplication of the element
as2 and as1)
promoter MPr1111"

BASE COUNT 94 a 74 c 45 g 83 t
ORIGIN

Query Match 73.0%; Score 46; DB 6; Length 296;
Best Local Similarity 100.0%; Pred. No. 4.7e-07;
Matches 46; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 18 GATTGATGATATCTCCACTGACGTAAAGGATGACGATGCCACT 63
Db 42 GATTGATGATATCTCCACTGACGTAAAGGATGACGATGCCACT 87

RESULT 13
LOCUS AX036739 371 bp DNA linear PAT 16-NOV-2000
DEFINITION Sequence 5 from Patent WO0058485.
ACCESSION AX036739
VERSION AX036739.1 GI:11226248
KEYWORDS
SOURCE
ORGANISM
synthetic construct.
artificial sequences.
REFERENCE 1 (bases 1 to 371)
AUTHORS Rance, I., Theisen, M. and Gruber, V.
TITLE Chimeric expression promoters originating from commelina yellow
mottle virus and cassava vein mosaic virus
PATENT: WO 0058485-A 5 05-OCT-2000;
JOURNAL MERISTEM THERAPEUTICS (FR) ; RANCE IANN (FR) ; THEISEN MANFRED (FR)
FEATURES
source
1. .371
/organism="synthetic construct"
/db_xref="taxon:32630"
/note="Promoter MPr1146"

BASE COUNT 122 a 68 c 89 g 92 t
ORIGIN

Query Match 73.0%; Score 46; DB 6; Length 371;
Best Local Similarity 100.0%; Pred. No. 4.7e-07;

Matches 46; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 18 GATTGATGTGATATCTCCAGCTAGGATGAGCATGCCACT 63
 DB 93 GATTGATGTGATATCTCCAGCTAGGATGAGCATGCCACT 138

DB 258 GATTGATGTGATATCTCCAGCTAGGATGAGCATGCCACT 302

Search completed: May 24, 2003, 14:52:24
 Job time : 352.903 secs

RESULT 14
 AX036755/c
 LOCUS AX036755 392 bp DNA linear PAT 16-NOV-2000
 DEFINITION Sequence 21 from Patent WO058485.
 ACCESSION AX036755
 VERSION AX036755.1 GI:11226264
 KEYWORDS
 SOURCE synthetic construct.
 ORGANISM synthetic construct.
 artificial sequences.

REFERENCE 1 (bases 1 to 392)
 AUTHORS Rance,I., Theisen,M. and Gruber,V.
 TITLE Chimeric expression promoters originating from commelina yellow
 JOURNAL mottle virus and cassava vein mosaic virus
 Patent: WO 0058485-A 21-05-OCT-2000;
 MERISTEM THERAPEUTICS (FR) ; RANCE IANN (FR) ; THEISEN MANFRED (FR)
 ; GRUBER VERONIQUE (FR)
 FEATURES
 source Location/Qualifiers
 1..392
 /organism="synthetic construct"
 /db_xref="taxon:32630"
 /note="Promoter MPr1164"

Promoter 127 a 80 c 87 g 98 t
 BASE COUNT
 ORIGIN

Query Match 71.4%; Score 45; DB 6; Length 392;
 Best Local Similarity 100.0%; Pred. No. 1.2e-06;
 Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 18 GATTGATGTGATATCTCCAGCTAGGATGAGCATGCCACT 62
 DB 278 GATTGATGTGATATCTCCAGCTAGGATGAGCATGCCACT 234

RESULT 15
 AX036753
 LOCUS AX036753 393 bp DNA linear PAT 16-NOV-2000
 DEFINITION Sequence 19 from Patent WO058485.
 ACCESSION AX036753
 VERSION AX036753.1 GI:11226262
 KEYWORDS
 SOURCE synthetic construct.
 ORGANISM synthetic construct.
 artificial sequences.

REFERENCE 1 (bases 1 to 393)
 AUTHORS Rance,I., Theisen,M. and Gruber,V.
 TITLE Chimeric expression promoters originating from commelina yellow
 JOURNAL mottle virus and cassava vein mosaic virus
 Patent: WO 0058485-A 19-05-OCT-2000;
 MERISTEM THERAPEUTICS (FR) ; RANCE IANN (FR) ; THEISEN MANFRED (FR)
 ; GRUBER VERONIQUE (FR)
 FEATURES
 source Location/Qualifiers
 1..393
 /organism="synthetic construct"
 /db_xref="taxon:32630"
 /note="Promoter MPr1162"

Promoter 128 a 75 c 93 g 97 t
 BASE COUNT
 ORIGIN

Query Match 71.4%; Score 45; DB 6; Length 393;
 Best Local Similarity 100.0%; Pred. No. 1.2e-06;
 Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 18 GATTGATGTGATATCTCCAGCTAGGATGAGCATGCCACT 62

GenCore version 5.1.4.p5.4578
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OM nucleic - nucleic search, using sw model

Run on: May 24, 2003, 07:18:51 ; Search time 108.726 Seconds
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Gapop 10.0 , Gapext 1.0

Searched: 2185239 seqs, 112599159 residues

Total number of hits satisfying chosen parameters: 4370478

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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24: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA2002.DAT.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	63	100.0	63 21 AAA96847	Directional desoxy
2	63	100.0	63 21 AAA96471	Nucleotide sequenc
3	59	93.7	280 21 AAA96463	Nucleotide sequenc
4	59	93.7	301 21 AAA96841	Nucleotide sequenc
5	59	93.7	398 21 AAA96840	Nucleotide sequenc
6	59	93.7	472 21 AAA96859	Nucleotide sequenc
7	59	93.7	541 21 AAA96858	Nucleotide sequenc
8	59	93.7	604 21 AAA96857	Nucleotide sequenc
9	46	73.0	79 21 AAA96846	Directional desoxy

10	46	73.0	79 21 AAA96472	Nucleotide sequenc
11	46	73.0	259 21 AAA96477	Nucleotide sequenc
12	46	73.0	296 21 AAA96465	Nucleotide sequenc
13	46	73.0	371 21 AAA96839	Nucleotide sequenc
14	45	71.4	392 21 AAA96855	Nucleotide sequenc
15	45	71.4	393 21 AAA96853	Nucleotide sequenc
16	45	71.4	462 21 AAA96854	Nucleotide sequenc
17	45	71.4	600 21 AAA96856	Nucleotide sequenc
18	43.4	68.9	189 22 AAD10066	Amplified product
19	43.4	68.9	240 21 AAA71895	Soybean RRS gene N
20	43.4	68.9	309 21 AAC87192	Camv35S promoter e
21	43.4	68.9	309 22 AAD33764	Caulliflower mosaic
22	43.4	68.9	333 22 AAC83764	Plasmid pMON295 Ca
23	43.4	68.9	334 22 AAH28369	Nucleotide sequenc
24	43.4	68.9	338 20 AAH99492	Caulliflower mosaic
25	43.4	68.9	350 13 AAQ23533	Camv35S promoter (
26	43.4	68.9	352 13 AAQ25080	Camv 35S promoter,
27	43.4	68.9	395 15 AAQ72688	Caulliflower mosaic
28	43.4	68.9	396 17 AAT33299	Nucleotide sequenc
29	43.4	68.9	396 22 AAH28368	Nucleotide sequenc
30	43.4	68.9	400 20 AAH99491	Sequence containin
31	43.4	68.9	444 20 AAH86466	35S CMV promoter s
32	43.4	68.9	444 22 AAC89658	Tomato spotted wil
33	43.4	68.9	446 20 AAC89658	35S-omega CMV prom
34	43.4	68.9	446 22 AAC89660	Tomato spotted wil
35	43.4	68.9	470 21 AAA51890	Chimeric CAMV35S-
36	43.4	68.9	522 24 AAD39449	FMV35S90 enhancer
37	43.4	68.9	532 21 AAA75458	Nucleotide sequenc
38	43.4	68.9	532 22 AAD06306	CMV 35S promoter o
39	43.4	68.9	532 22 AAD06360	Camv 35S promoter
40	43.4	68.9	532 22 AAF89817	Nucleotide sequenc
41	43.4	68.9	532 22 AAF89826	Nucleotide sequenc
42	43.4	68.9	532 24 ABL57432	Caulliflower mosaic
43	43.4	68.9	550 24 AAD34678	Camv 35S promoter
44	43.4	68.9	560 21 AAA75462	Nucleotide sequenc
45	43.4	68.9	560 22 AAD06310	CMV 35S promoter o

ALIGNMENTS

RESULT 1	
AAA96847	AAA96847 standard; DNA; 63 BP.
AC	AAA96847;
XX	
XX	19-FEB-2001 (first entry)
DT	
XX	
DE	Directional desoxynucleotide building block S6.
XX	
XX	Promoter; intergenic region; Commelina yellow mottle virus;
KW	Chimeric expression promoter; plant vascular expression promoter;
KW	plant green tissue expression promoter; Cassava vein mosaic virus;
KW	transgenic plant; ss.
OS	Synthetic.
XX	
PN	WO200058485-A1.
XX	
PD	05-OCT-2000.
XX	
PF	29-MAR-2000; 2000WO-1B00370.
XX	
PR	29-MAR-1999; 99FR-0003925.
XX	
PA	(MERI-) MERISTEM THERAPEUTICS.
XX	
PI	Rance I, Gruber V, Theisen M;
XX	
DR	WPI: 2000-647238/62.
XX	
PT	Chimeric expression promoter for transgenic plant production, comprises

PT sequence from promoter comprising vascular expression region replaced
 PT with sequence from promoter comprising green tissue expression region
 XX
 XX Disclosure: Page 30; 91pp; English.
 CC The present sequence represents a directional desoxynucleotide building
 CC block, which was used to construct chimeric promoters of the invention.
 CC The specification describes chimeric expression promoters. These
 CC chimeric promoters comprise a nucleic acid sequence which is derived
 CC from a first plant promoter, in which a plant vascular expression
 CC promoter region is replaced with a nucleic acid sequence derived from
 CC a second plant promoter comprising a plant green tissue expression
 CC promoter region. Preferably, the first plant promoter originates from
 CC Comellina yellow mottle virus, and the second plant promoter originates
 CC from the Cassava vein mosaic virus. Especially, the promoters are
 CC derived from intergenic regions. The chimeric promoters are useful
 CC for producing transgenic plants.
 XX
 SQ Sequence 63 BP; 16 A; 14 C; 17 G; 16 T; 0 other;
 Query Match 100.0%; Score 63; DB 21; Length 63;
 Best Local Similarity 100.0%; Pred. No. 2.4e-15;
 Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CATGCTGCACAGTACGTGATGTGATATCTCCACTGACGTAAGGATGACGCATGCC 60
 DB 1 CATGCTGCACAGTACGTGATGTGATATCTCCACTGACGTAAGGATGACGCATGCC 60
 QY 61 ACT 63
 DB 61 ACT 63
 DE Nucleotide sequence of the promoter Mpr1108.
 DE Nucleotide sequence of the directional building block S6.
 XX
 KW pete promoter; chimeric promoter; transgenic plant; Mpr1108;
 KW plastocyanin gene promoter; PCR primer; ss.
 XX
 OS Synthetic.
 XX WO200056906-A1.
 PN 28-SEP-2000.
 PD 20-MAR-2000; 2000WO-IB00317.
 PF 22-MAR-1999; 99FR-0003635.
 PR (MERI-) MERISTEM THERAPEUTICS.
 PA Rance I, Gruber V, Theisen M;
 PI WPI; 2000-587667/55.
 DR Chimeric expression promoter for producing dicotyledonous and
 PT monocotyledonous transgenic plants comprises a nucleic acid sequence
 PT derived from a promoter of the pea plastocyanin gene -
 XX
 PS Claim 24; Page 75; 83pp; English.
 CC The present sequence represents the directional building block S6,
 CC which is used to construct chimeric promoters of the invention in
 CC PCR reactions. The specification describes a chimeric expression
 CC promoter comprising a pete promoter of the pea plastocyanin gene, or

CC comprising a G box operably or functionally linked upstream of a
 CC CAAT box, TATA box and transcription initiation site. The chimeric
 CC promoters are used in expression vectors for producing transgenic
 CC plants, such as dicotyledonous species, e.g. potato, tobacco, cotton,
 CC lettuce, tomato, melon, cucumber, pea, rape, beetroot, or sunflower,
 CC and monocotyledonous species, e.g. wheat, barley, oat, rice, or corn.
 XX
 SQ Sequence 63 BP; 16 A; 14 C; 17 G; 16 T; 0 other;
 Query Match 100.0%; Score 63; DB 21; Length 63;
 Best Local Similarity 100.0%; Pred. No. 2.4e-15;
 Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CATGCTGCACAGTACGTGATGTGATATCTCCACTGACGTAAGGATGACGCATGCC 60
 DB 1 CATGCTGCACAGTACGTGATGTGATATCTCCACTGACGTAAGGATGACGCATGCC 60
 QY 61 ACT 63
 DB 61 ACT 63
 DE Nucleotide sequence of the promoter Mpr1110.
 DE Nucleotide sequence of the promoter Mpr1110;
 KW pete promoter; chimeric promoter; transgenic plant; Mpr1110;
 KW plastocyanin gene promoter; ss.
 XX
 OS Synthetic.
 OS Pisum sativum.
 OS WO200056906-A1.
 PN 28-SEP-2000.
 PD 20-MAR-2000; 2000WO-IB00317.
 PF 22-MAR-1999; 99FR-0003635.
 PR (MERI-) MERISTEM THERAPEUTICS.
 PA Rance I, Gruber V, Theisen M;
 PI WPI; 2000-587667/55.
 DR Chimeric expression promoter for producing dicotyledonous and
 PT monocotyledonous transgenic plants comprises a nucleic acid sequence
 PT derived from a promoter of the pea plastocyanin gene -
 XX
 PS Claim 2; Page 70; 83pp; English.
 CC The present sequence represents the chimeric promoter Mpr1110. The
 CC promoter is derived from the pete promoter from pea plastocyanin gene,
 CC by fusing the pete as-1 like and nos enhancer like elements to the
 CC promoter Mpr1098 (comprising TATA and CAAT boxes of pete) and then
 CC inserting a G box and fusing a Fragment of 35S RNA of CMV. The pete
 CC promoter directs cell-specific but not full light-regulated expression in
 CC transgenic tobacco plants. The promoter is used to construct chimeric
 CC promoters of the invention. The specification describes a chimeric
 CC expression promoter comprising a promoter of the pea plastocyanin gene,
 CC or comprising a G box operably or functionally linked upstream of a CAAT
 CC box, TATA box and transcription initiation site. The chimeric promoters
 CC are used in expression vectors for producing transgenic plants, such as
 CC dicotyledonous species, e.g. potato, tobacco, cotton, lettuce, tomato,
 CC melon, cucumber, pea, rape, beetroot, or sunflower, and monocotyledonous
 CC species, e.g. wheat, barley, oat, rice, or corn.

De Nucleotide sequence of chimeric expression promoter pM1109
XX

KW Promoter: intergenic region; Commelina yellow mottle virus;
KM chimeric expression promoter; plant vascular expression promoter;
KM plant green tissue expression promoter; Cassava vein mosaic virus;
KM transgenic plant; chimera; ss.
XX
OS Chimeric - Commelina yellow mottle virus.
OS Chimeric - Cassava vein mosaic virus.
XX
PN WO200058485-A1.
XX
PD 05-OCT-2000.
XX
PF 29-MAR-2000; 2000MO-IB00370.
XX
PR 29-MAR-1999; 99FR-0003925.
XX
PA (MERI-) MERISTEM THERAPEUTICS.
XX
PI Rance I, Gruber V, Theisen M;
XX
DR WPI; 2000-647238/62.
XX
PT Chimeric expression promoter for transgenic plant production, comprises
PT sequence from promoter comprising vascular expression region replaced
PT with sequence from promoter comprising green tissue expression region
XX
PS Claim 5; Page 88; 91pp; English.
XX
CC The present sequence represents a chimeric promoter of the invention.
CC The specification describes chimeric expression promoters. These
CC chimeric promoters comprise a nucleic acid sequence which is derived
CC from a first plant promoter, in which a plant vascular expression
CC promoter region is replaced with a nucleic acid sequence derived from
CC a second plant promoter comprising a plant green tissue expression
CC promoter region. Preferably, the first plant promoter originates from
CC Commelina yellow mottle virus, and the second plant promoter originates
CC from the Cassava vein mosaic virus. Especially, the promoters are
CC derived from intergenic regions. The chimeric promoters are useful
CC for producing transgenic plants.
XX
SQ Sequence 472 BP; 149 A; 92 C; 112 G; 119 T; 0 other;
XX
Query Match 93.7%; Score 59; DB 21; Length 472;
Best Local Similarity 100.0%; Pred. No. 1.6e-13;
Matches 59; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
OY 5 CTCGACACTAGTGGATTGATGTATATCTCCACTGACGTAAAGGATGACGATGCCACT 63
DB 110 CTCGACACTAGTGGATTGATGTATATCTCCACTGACGTAAAGGATGACGATGCCACT 168
XX
RESULT 7
AAA96858
ID AAA96858 standard; DNA: 541 BP.
XX
AC AAA96858;
XX
DT 19-FEB-2001 (first entry)
XX
DE Nucleotide sequence of chimeric expression promoter MPr1168.
XX
KM Promoter: intergenic region; Commelina yellow mottle virus;
KM chimeric expression promoter; plant vascular expression promoter;
KM plant green tissue expression promoter; Cassava vein mosaic virus;
KM transgenic plant; chimera; ss.
XX
OS Chimeric - Commelina yellow mottle virus.
OS Chimeric - Cassava vein mosaic virus.
XX
PN WO200058485-A1.
XX
PD 05-OCT-2000.

XX
PF 29-MAR-2000; 2000MO-IB00370.
XX
PR 29-MAR-1999; 99FR-0003925.
XX
PA (MERI-) MERISTEM THERAPEUTICS.
XX
PI Rance I, Gruber V, Theisen M;
XX
DR WPI; 2000-647238/62.
XX
PT Chimeric expression promoter for transgenic plant production, comprises
PT sequence from promoter comprising vascular expression region replaced
PT with sequence from promoter comprising green tissue expression region
XX
PS Claim 5; Page 87-88; 91pp; English.
XX
CC The present sequence represents a chimeric promoter of the invention.
CC The specification describes chimeric expression promoters. These
CC chimeric promoters comprise a nucleic acid sequence which is derived
CC from a first plant promoter, in which a plant vascular expression
CC promoter region is replaced with a nucleic acid sequence derived from
CC a second plant promoter comprising a plant green tissue expression
CC promoter region. Preferably, the first plant promoter originates from
CC Commelina yellow mottle virus, and the second plant promoter originates
CC from the Cassava vein mosaic virus. Especially, the promoters are
CC derived from intergenic regions. The chimeric promoters are useful
CC for producing transgenic plants.
XX
SQ Sequence 541 BP; 169 A; 104 C; 130 G; 138 T; 0 other;
XX
Query Match 93.7%; Score 59; DB 21; Length 541;
Best Local Similarity 100.0%; Pred. No. 1.7e-13;
Matches 59; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
OY 5 CTCGACACTAGTGGATTGATGTATATCTCCACTGACGTAAAGGATGACGATGCCACT 63
DB 110 CTCGACACTAGTGGATTGATGTATATCTCCACTGACGTAAAGGATGACGATGCCACT 168
XX
RESULT 8
AAA96857
ID AAA96857 standard; DNA: 604 BP.
XX
AC AAA96857;
XX
DT 19-FEB-2001 (first entry)
XX
DE Nucleotide sequence of chimeric expression promoter MPr1167.
XX
KM Promoter: intergenic region; Commelina yellow mottle virus;
KM chimeric expression promoter; plant vascular expression promoter;
KM plant green tissue expression promoter; Cassava vein mosaic virus;
KM transgenic plant; chimera; ss.
XX
OS Chimeric - Commelina yellow mottle virus.
OS Chimeric - Cassava vein mosaic virus.
XX
PN WO200058485-A1.
XX
PD 05-OCT-2000.
XX
PF 29-MAR-2000; 2000MO-IB00370.
XX
PR 29-MAR-1999; 99FR-0003925.
XX
PA (MERI-) MERISTEM THERAPEUTICS.
XX
PI Rance I, Gruber V, Theisen M;
XX
DR WPI; 2000-647238/62.

PT Chimeric expression promoter for transgenic plant production, comprises
PT sequence from promoter comprising vascular expression region replaced
PT with sequence from promoter comprising green tissue expression region
PT
PS Claim 5; Page 87; 91pp: English.
XX
XX The present sequence represents a chimeric promoter of the invention.
CC The specification describes chimeric expression promoters. These
CC chimeric promoters comprise a nucleic acid sequence which is derived
CC from a first plant promoter, in which a plant vascular expression
CC promoter region is replaced with a nucleic acid sequence derived from
CC a second plant promoter comprising a plant green tissue expression
CC promoter region. Preferably, the first plant promoter originates from
CC Commelina yellow mottle virus, and the second plant promoter originates
CC from the Cassava vein mosaic virus. Especially, the promoters are
CC derived from intergenic regions. The chimeric promoters are useful
CC for producing transgenic plants.
XX
SQ Sequence 604 BP; 186 A; 116 C; 145 G; 157 T; 0 other;
Query Match 93.7%; Score 59; DB 21; Length 604;
Best Local Similarity 100.0%; Pred. No. 1.7e-13;
Matches 59; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 5 CTGCAGACTAGTGATGATGATCTCCACTGACGTAGGAGTACGCATGCCACT 63
DB 110 CTGCAGACTAGTGATGATGATGATCTCCACTGACGTAGGAGTACGCATGCCACT 168
RESULT 9
AAA96848
ID AAA96848 standard; DNA; 79 BP.
XX
AC AAA96848;
XX
DT 19-FEB-2001 (first entry)
XX
DE Directional desoxynucleotide building block S7.
XX
XX Promoter; Intergenic region; Commelina yellow mottle virus;
KM chimeric expression promoter; plant vascular expression promoter;
KM plant green tissue expression promoter; Cassava vein mosaic virus;
KM transgenic plant; ss.
XX
XX Synthetic.
XX
PN WO200058485-A1.
XX
XX 05-OCT-2000.
XX
PF 29-MAR-2000; 2000WO-IB00370.
XX
XX 29-MAR-1999; 99FR-0003925.
XX
PA (MERI-) MERISTEM THERAPEUTICS.
XX
PI Rance I, Gruber V, Theisen M;
XX
DR WPI; 2000-647238/62.
XX
PT Chimeric expression promoter for transgenic plant production, comprises
PT sequence from promoter comprising vascular expression region replaced
PT with sequence from promoter comprising green tissue expression region
PT
XX
XX Disclosure; Page 26; 91pp: English.
XX
XX The present sequence represents a directional desoxynucleotide building
CC block, which was used to construct chimeric promoters of the invention.
CC The specification describes chimeric expression promoters. These
CC chimeric promoters comprise a nucleic acid sequence which is derived
CC from a first plant promoter, in which a plant vascular expression

CC promoter region is replaced with a nucleic acid sequence derived from
CC a second plant promoter comprising a plant green tissue expression
CC promoter region. Preferably, the first plant promoter originates from
CC Commelina yellow mottle virus, and the second plant promoter originates
CC from the Cassava vein mosaic virus. Especially, the promoters are
CC derived from intergenic regions. The chimeric promoters are useful
CC for producing transgenic plants.
XX
SQ Sequence 79 BP; 22 A; 15 C; 20 G; 22 T; 0 other;
Query Match 73.0%; Score 46; DB 21; Length 79;
Best Local Similarity 100.0%; Pred. No. 1.3e-08;
Matches 46; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 18 GATGATGTGATATCTCCACTGACGTAGGAGTACGCATGCCACT 63
DB 34 GATGATGTGATATCTCCACTGACGTAGGAGTACGCATGCCACT 79
RESULT 10
AAA96472
ID AAA96472 standard; DNA; 79 BP.
XX
AC AAA96472;
XX
DT 08-FEB-2001 (first entry)
XX
DE Nucleotide sequence of the directional building block S7.
XX
XX pete promoter; chimeric promoter; transgenic plant; Mpr1108;
KM plastocyanin gene promoter; PCR primer; ss.
XX
XX Synthetic.
XX
PN WO200056906-A1.
XX
XX 28-SEP-2000.
XX
PF 20-MAR-2000; 2000WO-IB00317.
XX
XX 22-MAR-1999; 99FR-0003635.
XX
PA (MERI-) MERISTEM THERAPEUTICS.
XX
PI Rance I, Gruber V, Theisen M;
XX
DR WPI; 2000-587667/55.
XX
PT Chimeric expression promoter for producing dicotyledonous and
PT monocotyledonous transgenic plants comprises a nucleic acid sequence
PT derived from a promoter of the pea plastocyanin gene
PT
XX
XX Claim 24; Page 76; 83pp: English.
XX
XX The present sequence represents the directional building block S7,
CC which is used to construct chimeric promoters of the invention in
CC PCR reactions. The specification describes a chimeric expression
CC promoter comprising a pete promoter of the pea plastocyanin gene, or
CC comprising a G box operably or functionally linked upstream of a
CC CAT box, TATA box and transcription initiation site. The chimeric
CC promoters are used in expression vectors for producing transgenic
CC plants, such as dicotyledonous species, e.g. potato, tobacco, cotton,
CC lettuce, tomato, melon, cucumber, pea, rape, beetroot, or sunflower,
CC and monocotyledonous species, e.g. wheat, barley, oat, rice, or corn.
XX
SQ Sequence 79 BP; 22 A; 15 C; 20 G; 22 T; 0 other;
Query Match 73.0%; Score 46; DB 21; Length 79;
Best Local Similarity 100.0%; Pred. No. 1.3e-08;
Matches 46; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 18 GATGATGTGATATCTCCACTGACGTAGGAGTACGCATGCCACT 63
DB 34 GATGATGTGATATCTCCACTGACGTAGGAGTACGCATGCCACT 79

DB 34 GATTGATGATATCTCCACTGACGTAAAGGAGCAGCATGCCACT 79

RESULT 11
 ID AAA96477 standard; DNA: 259 BP.
 XX AAA96477;
 AC AAA96477;
 XX 08-FEB-2001 (first entry)
 DT 08-FEB-2001 (first entry)

Nucleotide sequence of the promoter Mp1112.
 DE pete promoter; chimeric promoter; transgenic plant; Mp1112;
 KW plastocyanin gene promoter; ss.
 XX Plasm salivum.
 OS WO200056906-A1.
 XX 28-SEP-2000.
 PD 20-MAR-2000; 2000WO-IB00317.
 PF 22-MAR-1999; 99FR-0003635.
 PR (MERI-) MERISTEM THERAPEUTICS.
 XX Rance I, Gruber V, Theisen M;
 PI MPI; 2000-587667/55.
 DR Chimeric expression promoter for producing dicotyledonous and
 PT monocotyledonous transgenic plants comprising a nucleic acid sequence
 PT derived from a promoter of the pea plastocyanin gene
 XX Claim 25; Page 79; 83pp; English.

The present sequence represents the chimeric promoter Mp1112. The
 CC promoter is derived from the pete promoter from pea plastocyanin gene,
 CC by fusing the pete as-1 like and nos enhancer like elements to the
 CC promoter Mp1098 (comprising TATA and CAAT boxes of pete), and then
 CC fusing a fragment comprising a duplication of the element as2 and as1.
 CC The pete promoter directs cell-specific but not full light-regulated
 CC expression in transgenic tobacco plants. The promoter is used to
 CC construct chimeric promoters of the invention. The specification
 CC describes a chimeric expression promoter comprising a promoter of
 CC the pea plastocyanin gene, or comprising a G box operably or
 CC functionally linked upstream of a CAAT box, TATA box and transcription
 CC initiation site. The chimeric promoters are used in expression vectors
 CC for producing transgenic plants, such as dicotyledonous species,
 CC e.g. potato, tobacco, cotton, lettuce, tomato, melon, cucumber, pea,
 CC rape, beetroot, or sunflower, and monocotyledonous species, e.g. wheat,
 CC barley, oat, rice, or corn.

Sequence 259 BP; 82 A; 67 C; 38 G; 72 T; 0 other;

Query Match 73.0%; Score 46; DB 21; Length 259;
 Best Local Similarity 100.0%; Pred. No. 1.9e-08;
 Matches 46; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 18 GATTGATGATATCTCCACTGACGTAAAGGAGCAGCATGCCACT 63
 DB 42 GATTGATGATATCTCCACTGACGTAAAGGAGCAGCATGCCACT 87

RESULT 12
 ID AAA96465 standard; DNA: 296 BP.
 AC AAA96465;
 XX 08-FEB-2001 (first entry)

XX Nucleotide sequence of the promoter Mp1111.
 DE pete promoter; chimeric promoter; transgenic plant; Mp1111;
 KW plastocyanin gene promoter; ss.
 XX Synthetic.
 OS Plasm salivum.
 XX WO200056906-A1.
 XX 28-SEP-2000.
 PD 20-MAR-2000; 2000WO-IB00317.
 PF 22-MAR-1999; 99FR-0003635.
 PR (MERI-) MERISTEM THERAPEUTICS.
 XX Rance I, Gruber V, Theisen M;
 PI MPI; 2000-587667/55.
 DR Chimeric expression promoter for producing dicotyledonous and
 PT monocotyledonous transgenic plants comprising a nucleic acid sequence
 PT derived from a promoter of the pea plastocyanin gene
 XX Claim 2; Page 71; 83pp; English.

The present sequence represents the chimeric promoter Mp1111. The
 CC promoter is derived from the pete promoter from pea plastocyanin gene,
 CC by fusing the pete as-1 like and nos enhancer like elements to the
 CC promoter Mp1098 (comprising TATA and CAAT boxes of pete), and then
 CC inserting a G box and fusing a fragment comprising a duplication of the
 CC element as2 and as1. The pete promoter directs cell-specific but not
 CC full light-regulated expression in transgenic tobacco plants. The
 CC promoter is used to construct chimeric promoters of the invention. The
 CC specification describes a chimeric expression promoter comprising a
 CC promoter of the pea plastocyanin gene, or comprising a G box operably
 CC or functionally linked upstream of a CAAT box, TATA box and transcription
 CC initiation site. The chimeric promoters are used in expression vectors
 CC for producing transgenic plants, such as dicotyledonous species,
 CC e.g. potato, tobacco, cotton, lettuce, tomato, melon, cucumber, pea,
 CC rape, beetroot, or sunflower, and monocotyledonous species, e.g. wheat,
 CC barley, oat, rice, or corn.

Sequence 296 BP; 94 A; 74 C; 45 G; 83 T; 0 other;

Query Match 73.0%; Score 46; DB 21; Length 296;
 Best Local Similarity 100.0%; Pred. No. 2e-08;
 Matches 46; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 18 GATTGATGATATCTCCACTGACGTAAAGGAGCAGCATGCCACT 63
 DB 42 GATTGATGATATCTCCACTGACGTAAAGGAGCAGCATGCCACT 87

RESULT 13
 ID AAA96839 standard; DNA: 371 BP.
 AC AAA96839;
 XX 19-FEB-2001 (first entry)

Nucleotide sequence of chimeric expression promoter Mp1146.
 DE Promoter; intergenic region; Commelina yellow mottle virus;
 KW chimeric expression promoter; plant vascular expression promoter;
 KW plant green tissue expression promoter; Cassava vein mosaic virus;
 KW transgenic plant; chimera; ss.
 XX Chimeric - Commelina yellow mottle virus.

OS Chimeric - Cassava vein mosaic virus.
XX
PN WO200058485-A1.
XX
PD 05-OCT-2000.
XX
PF 29-MAR-2000; 2000WO-IB00370.
XX
PR 29-MAR-1999; 99FR-0003925.
XX
PA (MERIT-) MERISTEM THERAPEUTICS.
XX
PI Rance I, Gruber V, Theisen M;
XX
DR WPI: 2000-647238/62.
XX
PT Chimeric expression promoter for transgenic plant production, comprises
PT sequence from promoter comprising vascular expression region replaced
PT with sequence from promoter comprising green tissue expression region
XX
XX
PS Claim 5; Page 81; 91pp; English.
XX
CC The present sequence represents a chimeric promoter of the invention.
CC The specification describes chimeric expression promoters. These
CC chimeric promoters comprise a nucleic acid sequence which is derived
CC from a first plant promoter, in which a plant vascular expression
CC promoter region is replaced with a nucleic acid sequence derived from
CC a second plant promoter comprising a plant green tissue expression
CC promoter region. Preferably, the first plant promoter originates from
CC Commelina yellow mottle virus, and the second plant promoter originates
CC from the Cassava vein mosaic virus. Especially, the promoters are
CC derived from intergenic regions. The chimeric promoters are useful
CC for producing transgenic plants.
XX
SQ Sequence 371 BP; 122 A; 68 C; 89 G; 92 T; 0 other;
XX
Query Match 73.0%; Score 46; DB 21; Length 371;
Best Local Similarity 100.0%; Pred. No. 2.1e-08;
Matches 46; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 18 GATTGATGTGATATCTCCACGTAGGATGATGCGATGCCACT 63
DB 93 GATTGATGTGATATCTCCACGTAGGATGATGCGATGCCACT 138
XX
RESULT 14
AAA96855/c
ID AAA96855 standard; DNA; 392 BP.
XX
AC AAA96855;
XX
DT 19-FEB-2001 (first entry)
XX
DE Nucleotide sequence of chimeric expression promoter MPr1164.
XX
KW Promoter; intergenic region; Commelina yellow mottle virus;
KW chimeric expression promoter; plant vascular expression promoter;
KW plant green tissue expression promoter; Cassava vein mosaic virus;
KW transgenic plant; chimera; ss.
XX
OS Chimeric - Commelina yellow mottle virus.
OS Chimeric - Cassava vein mosaic virus.
XX
PN WO200058485-A1.
XX
PD 05-OCT-2000.
XX
PF 29-MAR-2000; 2000WO-IB00370.
XX
PR 29-MAR-1999; 99FR-0003925.
XX
PA (MERIT-) MERISTEM THERAPEUTICS.

XX
PI Rance I, Gruber V, Theisen M;
XX
DR WPI: 2000-647238/62.
XX
PT Chimeric expression promoter for transgenic plant production, comprises
PT sequence from promoter comprising vascular expression region replaced
PT with sequence from promoter comprising green tissue expression region
XX
XX
PS Claim 5; Page 86; 91pp; English.
XX
CC The present sequence represents a chimeric promoter of the invention.
CC The specification describes chimeric expression promoters. These
CC chimeric promoters comprise a nucleic acid sequence which is derived
CC from a first plant promoter, in which a plant vascular expression
CC promoter region is replaced with a nucleic acid sequence derived from
CC a second plant promoter comprising a plant green tissue expression
CC promoter region. Preferably, the first plant promoter originates from
CC Commelina yellow mottle virus, and the second plant promoter originates
CC from the Cassava vein mosaic virus. Especially, the promoters are
CC derived from intergenic regions. The chimeric promoters are useful
CC for producing transgenic plants.
XX
SQ Sequence 392 BP; 127 A; 80 C; 87 G; 98 T; 0 other;
XX
Query Match 71.4%; Score 45; DB 21; Length 392;
Best Local Similarity 100.0%; Pred. No. 5.3e-08;
Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 18 GATTGATGTGATATCTCCACGTAGGATGATGCGATGCCAC 62
DB 278 GATTGATGTGATATCTCCACGTAGGATGATGCGATGCCAC 234
XX
RESULT 15
AAA96853
ID AAA96853 standard; DNA; 393 BP.
XX
AC AAA96853;
XX
DT 19-FEB-2001 (first entry)
XX
DE Nucleotide sequence of chimeric expression promoter MPr1162.
XX
KW Promoter; intergenic region; Commelina yellow mottle virus;
KW chimeric expression promoter; plant vascular expression promoter;
KW plant green tissue expression promoter; Cassava vein mosaic virus;
KW transgenic plant; chimera; ss.
XX
OS Chimeric - Commelina yellow mottle virus.
OS Chimeric - Cassava vein mosaic virus.
XX
PN WO200058485-A1.
XX
PD 05-OCT-2000.
XX
PF 29-MAR-2000; 2000WO-IB00370.
XX
PR 29-MAR-1999; 99FR-0003925.
XX
PA (MERIT-) MERISTEM THERAPEUTICS.
XX
PI Rance I, Gruber V, Theisen M;
XX
DR WPI: 2000-647238/62.
XX
PT Chimeric expression promoter for transgenic plant production, comprises
PT sequence from promoter comprising vascular expression region replaced
PT with sequence from promoter comprising green tissue expression region
XX
XX
PS Claim 5; Page 85; 91pp; English.

xx The present sequence represents a chimeric promoter of the invention.
cc The specification describes chimeric expression promoters. These
cc chimeric promoters comprise a nucleic acid sequence which is derived
cc from a first plant promoter, in which a plant vascular expression
cc promoter region is replaced with a nucleic acid sequence derived from
cc a second plant promoter comprising a plant green tissue expression
cc promoter region. Preferably, the first plant promoter originates from
cc *Commelina* yellow mottle virus, and the second plant promoter originates
cc from the *Cassava* vein mosaic virus. Especially, the promoters are
cc derived from intergenic regions. The chimeric promoters are useful
cc for producing transgenic plants.

5Q Sequence 393 BP; 128 A; 75 C; 93 G; 97 T; 0 other;

Query Match	71.48;	Score 45;	DB 21;	Length 393;
-------------	--------	-----------	--------	-------------

Best Local Similarity 100.0%; Pred. No. 5.3e-08;
Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
QY      18 GATTGATGTGATATCTCCACTGACGTAAGGGATGACCGATGCCAC   62
          |||
Db     258 GATTGATGTGATATCTCCACTGACGTAAGGGATGACCGATGCCAC   302
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Search completed: May 24, 2003, 14:34:44
Job time : 109.726 secs

GenCore version 5.1.4.p5.4578
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OM nucleic - nucleic search, using sw model

Run on: May 24, 2003, 13:52:01 ; Search time 26.0806 Seconds
(without alignments)
740.804 Million cell updates/sec

Title: US-09-963-803-13

Perfect score: 63
Sequence: 1 catgctgcagactagtgat.....aaggatgacatgacct 63

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 441362 seqs, 15338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued_Patents_NA.*
1: /cgn2_6/ptodata/1/ina/5A_COMB.seq.*
2: /cgn2_6/ptodata/1/ina/5B_COMB.seq.*
3: /cgn2_6/ptodata/1/ina/6A_COMB.seq.*
4: /cgn2_6/ptodata/1/ina/6B_COMB.seq.*
5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq.*
6: /cgn2_6/ptodata/1/ina/Backfile1.seq.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result	No.	Score	Query Match	Length	DB	ID	Description
1	43.4	68.9	439	1	US-08-247-809A-3	Sequence 3, Appl1	
2	43.4	68.9	439	2	US-08-711-728-3	Sequence 3, Appl1	
3	43.4	68.9	446	1	US-08-764-100-23	Sequence 23, Appl	
4	43.4	68.9	532	3	US-09-042-426-1	Sequence 1, Appl1	
5	43.4	68.9	532	4	US-09-291-238-1	Sequence 1, Appl1	
6	43.4	68.9	532	4	US-09-330-760-1	Sequence 1, Appl1	
7	43.4	68.9	532	4	US-09-328-473-1	Sequence 1, Appl1	
8	43.4	68.9	532	4	US-09-330-737-1	Sequence 1, Appl1	
9	43.4	68.9	532	4	US-09-329-169-1	Sequence 1, Appl1	
10	43.4	68.9	532	4	US-09-330-714A-1	Sequence 1, Appl1	
11	43.4	68.9	532	4	US-09-328-826-1	Sequence 1, Appl1	
12	43.4	68.9	560	3	US-09-042-426-5	Sequence 5, Appl1	
13	43.4	68.9	560	4	US-09-291-238-5	Sequence 5, Appl1	
14	43.4	68.9	560	4	US-09-330-760-5	Sequence 5, Appl1	
15	43.4	68.9	560	4	US-09-328-473-5	Sequence 5, Appl1	
16	43.4	68.9	560	4	US-09-330-737-5	Sequence 5, Appl1	
17	43.4	68.9	560	4	US-09-329-169-5	Sequence 5, Appl1	
18	43.4	68.9	560	4	US-09-330-714A-5	Sequence 5, Appl1	
19	43.4	68.9	560	4	US-09-328-826-5	Sequence 5, Appl1	
20	43.4	68.9	661	4	US-09-027-998A-33	Sequence 33, Appl	
21	43.4	68.9	793	1	US-08-371-764-1	Sequence 1, Appl1	
22	43.4	68.9	793	4	US-08-897-736-1	Sequence 1, Appl1	
23	43.4	68.9	831	1	US-08-450-834-5	Sequence 5, Appl1	
24	43.4	68.9	950	6	5177308-3	Patent No. 5177308	
25	43.4	68.9	978	1	US-08-446-486-31	Sequence 31, Appl	
26	43.4	68.9	978	1	US-08-463-308-31	Sequence 31, Appl	
27	43.4	68.9	979	1	US-08-446-486-30	Sequence 30, Appl	

28	43.4	68.9	979	1	US-08-463-308-30	Sequence 30, Appli
29	43.4	68.9	980	6	5254799-30	Patent No. 5254799
30	43.4	68.9	1030	1	US-07-936-163-46	Sequence 46, Appli
31	43.4	68.9	1030	4	US-08-729-601A-43	Sequence 43, Appli
32	43.4	68.9	1034	4	US-09-363-970-35	Sequence 35, Appli
33	43.4	68.9	1138	4	US-09-011-151-8	Sequence 8, Appli
34	43.4	68.9	1138	4	US-09-011-151-9	Sequence 9, Appli
35	43.4	68.9	1196	4	US-08-729-601A-46	Sequence 46, Appli
36	43.4	68.9	1279	4	US-09-185-244-2	Sequence 2, Appli
37	43.4	68.9	1279	4	US-09-471-913-6	Sequence 6, Appli
38	43.4	68.9	1303	3	US-08-894-440-2	Sequence 2, Appli
39	43.4	68.9	1303	4	US-09-458-093-2	Sequence 2, Appli
40	43.4	68.9	1651	3	US-09-065-999-5	Sequence 5, Appli
41	43.4	68.9	1651	3	US-09-065-999-6	Sequence 6, Appli
42	43.4	68.9	1722	1	US-08-247-809A-5	Sequence 5, Appli
43	43.4	68.9	1722	2	US-08-711-728-5	Sequence 5, Appli
44	43.4	68.9	1829	1	US-07-966-187-17	Sequence 17, Appli
45	43.4	68.9	1863	1	US-08-525-507-16	Sequence 16, Appli

ALIGNMENTS

RESULT 1
US-08-247-809A-3
; Sequence 3, Application US/08247809A
; Patent No. 5569823
; GENERAL INFORMATION:
; APPLICANT: Peter H. Schreier; Klaus Stenzel; Gunter Adam;
; APPLICANT: Edgar Maiss
; TITLE OF INVENTION: DEOXYRIBONUCLEIC ACIDS
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SPRUNG HORN KRAMER & WOODS
; STREET: 660 White Plains Road
; CITY: Tarrytown
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10591-5144
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 2.0 MB
; OPERATING SYSTEM: DOS
; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/247,809A
; FILING DATE: May 23, 1994
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: P 43 178 45.6 (Germany)
; FILING DATE: May 28, 1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Kurt G. Briscoe
; REGISTRATION NUMBER: 33,141
; REFERENCE/DOCKET NUMBER: Bayer 9049-KGB
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (914) 332-1700
; TELEFAX: (914) 332-1844
; TELEX:
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 439 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-08-247-809A-3

Query Match 68.9%; Score 43.4; DB 1; Length 439;
Best Local Similarity 97.8%; Pred. No. 4.3e-09;
Matches 44; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 12 CTAGTGGATGATGATGATCTCCACTGACGTAGGATGACGCA 56
DB 332 CAAGTGGATGATGATGATCTCCACTGACGTAGGATGACGCA 376

RESULT 2

US-08-711-728-3
Sequence 3, Application US/08711728
Patent No. 5973135
GENERAL INFORMATION:
APPLICANT: Peter H. Schreier; Klaus Stenzel; Gunter Adam;
APPLICANT: Edgar Maiss
TITLE OF INVENTION: DEOXYRIBONUCLEIC ACIDS
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSEE: SPRUNG HORN KRAMER & WOODS
STREET: 660 White Plains Road
CITY: Tarrytown
STATE: New York
COUNTRY: U.S.A.
ZIP: 10591-5144
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 2.0 MB
MEDIUM TYPE: Storage
COMPUTER: NEC Powermate 1 Plus
OPERATING SYSTEM: DOS
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/711,728
FILING DATE: 03-SEPT-1996
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/247,809
FILING DATE: 23-MAY-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE 43178456
FILING DATE: 28-MAY-1993
ATTORNEY/AGENT INFORMATION:
NAME: Kurt G. Briscoe
REGISTRATION NUMBER: 33,141
REFERENCE/DOCKET NUMBER: Bayer 9049.1-KGB
TELECOMMUNICATION INFORMATION:
TELEPHONE: (914) 332-1700
TELEFAX: (914) 332-1844
TELEX:
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 439 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-711-728-3

Query Match 68.9%; Score 43.4; DB 2; Length 439;
Best Local Similarity 97.8%; Pred. No. 4.3e-09;
Matches 44; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 12 CTAGTGGATGATGATGATCTCCACTGACGTAGGATGACGCA 56
DB 332 CAAGTGGATGATGATGATCTCCACTGACGTAGGATGACGCA 376

RESULT 3
US-08-764-100-23
Sequence 23, Application US/08764100
Patent No. 5773700
GENERAL INFORMATION:
APPLICANT: Van Grinsven J., Martinus O.
APPLICANT: De Haan, Petrus T.
APPLICANT: Giesen L., Johannes J.
APPLICANT: Peters, Dirk
APPLICANT: Goldbach, Robert W.

TITLE OF INVENTION: Improvements in or Relating to Organic
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sandoz Agro, Inc
STREET: 975 California Avenue
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/764,100
FILING DATE: 06-DEC-1996
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/214,064
FILING DATE:
APPLICATION NUMBER: US 08/032,235
FILING DATE: 17-MAR-1993
APPLICATION NUMBER: GB 9206016.9
FILING DATE: 19-MAR-1992
ATTORNEY/AGENT INFORMATION:
NAME: No. 57737001s, Allen E.
REGISTRATION NUMBER: 34,490
REFERENCE/DOCKET NUMBER: 137-1061
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 354-3592
TELEFAX: (415) 857-1125
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 446 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-764-100-23

Query Match 68.9%; Score 43.4; DB 1; Length 446;
Best Local Similarity 97.8%; Pred. No. 4.3e-09;
Matches 44; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 12 CTAGTGGATGATGATGATCTCCACTGACGTAGGATGACGCA 56
DB 268 CAAGTGGATGATGATGATCTCCACTGACGTAGGATGACGCA 312

RESULT 4
US-09-042-426-1
Sequence 1, Application US/09042426
Patent No. 6114608
GENERAL INFORMATION:
APPLICANT: Irvlin J. Mettler, Paul S. Dietrich, Ralph Sinibaldi
TITLE OF INVENTION: DNA Construct Containing Bacillus
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 6114608artis Corporation
STREET: 564 Morris Avenue
CITY: Summit
STATE: New Jersey
COUNTRY: USA
ZIP: 07901
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/042,426
FILING DATE: March 13, 1998

```

; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO

```

RESULT 7
US-09-328-473-1
; Sequence 1, Application US/09328473
; Patent No. 6232533

GENERAL INFORMATION:
APPLICANT: Irvn J. Mettler, Paul S. Dietrich, Ralph Sinibaldi
TITLE OF INVENTION: DNA Construct Containing Bacillus
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 6232534artis Corporation
STREET: 564 Morris Avenue
CITY: Summit
STATE: New Jersey
COUNTRY: USA
ZIP: 07901
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/328,473
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/042,426
FILING DATE: March 13, 1998
ATTORNEY/AGENT INFORMATION:
NAME: Hoxie, Thomas
REGISTRATION NUMBER: 32,993
REFERENCE/DOCKET NUMBER: 135/1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (919) 541-8614
TELEFAX: (919) 541-8689
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 532 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
IMMEDIATE SOURCE:
CLONE: 35S Promoter
US-09-328-473-1

Query Match 68.9%; Score 43.4; DB 4; Length 532;
Best Local Similarity 97.8%; Pred. No. 4.6e-09;
Matches 44; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 12 CTAAGTGGATGATGATATCTCCACTGACGTAGGATGACGCA 56
DB 268 CAAGTGGATGATGATATCTCCACTGACGTAGGATGACGCA 312

RESULT 8
US-09-330-737-1
Sequence 1, Application US/09330737
Patent No. 6232534
GENERAL INFORMATION:
APPLICANT: Irvn J. Mettler, Paul S. Dietrich, Ralph Sinibaldi
TITLE OF INVENTION: DNA Construct Containing Bacillus
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 6232534artis Corporation
STREET: 564 Morris Avenue
CITY: Summit
STATE: New Jersey
COUNTRY: USA
ZIP: 07901
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/330,737
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/042,426
FILING DATE: March 13, 1998
ATTORNEY/AGENT INFORMATION:
NAME: Hoxie, Thomas
REGISTRATION NUMBER: 32,993
REFERENCE/DOCKET NUMBER: 135/1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (919) 541-8614
TELEFAX: (919) 541-8689
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 532 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
IMMEDIATE SOURCE:
CLONE: 35S Promoter
US-09-330-737-1

Query Match 68.9%; Score 43.4; DB 4; Length 532;
Best Local Similarity 97.8%; Pred. No. 4.6e-09;
Matches 44; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 12 CTAAGTGGATGATGATATCTCCACTGACGTAGGATGACGCA 56
DB 268 CAAGTGGATGATGATATCTCCACTGACGTAGGATGACGCA 312

RESULT 9
US-09-329-169-1
Sequence 1, Application US/09329169
Patent No. 6329575
GENERAL INFORMATION:
APPLICANT: Irvn J. Mettler, Paul S. Dietrich, Ralph Sinibaldi
TITLE OF INVENTION: DNA Construct Containing Bacillus
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 6329575artis Corporation
STREET: 564 Morris Avenue
CITY: Summit
STATE: New Jersey
COUNTRY: USA
ZIP: 07901
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/329,169
FILING DATE: 09-Jun-1999
CLASSIFICATION: <unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/042,426
FILING DATE: <unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Hoxie, Thomas
REGISTRATION NUMBER: 32,993
REFERENCE/DOCKET NUMBER: 135/1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (919) 541-8614
TELEFAX: (919) 541-8689
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 532 base pairs
TYPE: nucleic acid

```

; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; IMMEDIATE SOURCE:
; CLONE: 35S Promoter
; SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-329-169-1

Query Match      68.9%; Score 43.4; DB 4; Length 532;
Best Local Similarity 97.8%; Pred. No. 4.6e-09;
Matches 44; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 12 CTAAGTGGATTGATGATATCTCCACTGACGTAAAGGATGACGCA 56
DB 268 CAAAGTGGATTGATGATATCTCCACTGACGTAAAGGATGACGCA 312

RESULT 10
; Sequence 1, Application US/09330714A
; Patent No. 6342660
; GENERAL INFORMATION:
; APPLICANT: Irvin J. Wettler, Paul S. Dietrich, Ralph Sinibaldi
; TITLE OF INVENTION: DNA Construct Containing Bacillus
; Thuringiensis Gene
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 6342660artis Corporation
; STREET: 564 Morris Avenue
; CITY: Summit
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07901
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/330,714A
; FILING DATE: 11-Jun-1999
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/042,426
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Hoxie, Thomas
; REGISTRATION NUMBER: 32,993
; REFERENCE/DOCKET NUMBER: 135/1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (919) 541-8614
; TELEFAX: (919) 541-8689
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 532 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; IMMEDIATE SOURCE:
; CLONE: 35S Promoter
; SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-330-714A-1

Query Match      68.9%; Score 43.4; DB 4; Length 532;
Best Local Similarity 97.8%; Pred. No. 4.6e-09;
Matches 44; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 12 CTAAGTGGATTGATGATATCTCCACTGACGTAAAGGATGACGCA 56
```

```

DB 268 CAAAGTGGATTGATGATATCTCCACTGACGTAAAGGATGACGCA 312

RESULT 11
; Sequence 1, Application US/09328826
; Patent No. 6399860
; GENERAL INFORMATION:
; APPLICANT: Irvin J. Wettler, Paul S. Dietrich, Ralph Sinibaldi
; TITLE OF INVENTION: DNA Construct Containing Bacillus
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 6399860artis Corporation
; STREET: 564 Morris Avenue
; CITY: Summit
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07901
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/328,826
; FILING DATE: 09-Jun-1999
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/042,426
; FILING DATE: March 13, 1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Hoxie, Thomas
; REGISTRATION NUMBER: 32,993
; REFERENCE/DOCKET NUMBER: 135/1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (919) 541-8614
; TELEFAX: (919) 541-8689
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 532 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; IMMEDIATE SOURCE:
; CLONE: 35S Promoter
; SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-328-826-1

Query Match      68.9%; Score 43.4; DB 4; Length 532;
Best Local Similarity 97.8%; Pred. No. 4.6e-09;
Matches 44; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 12 CTAAGTGGATTGATGATATCTCCACTGACGTAAAGGATGACGCA 56
DB 268 CAAAGTGGATTGATGATATCTCCACTGACGTAAAGGATGACGCA 312

RESULT 12
; Sequence 5, Application US/09042426
; Patent No. 6114608
; GENERAL INFORMATION:
; APPLICANT: Irvin J. Wettler, Paul S. Dietrich, Ralph Sinibaldi
; TITLE OF INVENTION: DNA Construct Containing Bacillus
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 6114608artis Corporation
; STREET: 564 Morris Avenue
; CITY: Summit
```

STATE: New Jersey
COUNTRY: USA
ZIP: 07901
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/042,426
FILING DATE: March 13, 1998
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Hoxie, Thomas
REGISTRATION NUMBER: 32,993
REFERENCE/DOCKET NUMBER: 135/1
TELEPHONE: (919) 541-8614
TELEFAX: (919) 541-8689
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 560 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
IMMEDIATE SOURCE:
CLONE: 35S Promoter
US-09-042-426-5

Query Match 68.9%; Score 43.4; DB 3; Length 560;
Best Local Similarity 97.8%; Pred. No. 4.7e-09;
Matches 44; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 12 CTAAGTGGATTGATGATATCTCCACTGACGTAAGGATGACGCA 56
DB 316 CAAGTGGATTGATGATATCTCCACTGACGTAAGGATGACGCA 360

RESULT 13
US-09-291-238-5
Sequence 5, Application US/09291238
Patent No. 6222104
GENERAL INFORMATION:
APPLICANT: Irvin J. Mettler, Paul S. Dietrich, Ralph Sinibaldi
TITLE OF INVENTION: DNA Construct Containing Bacillus
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 6222104artis Corporation
STREET: 564 Morris Avenue
CITY: Summit
STATE: New Jersey
COUNTRY: USA
ZIP: 07901
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/291,238
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/042,426
FILING DATE: March 13, 1998
ATTORNEY/AGENT INFORMATION:
NAME: Hoxie, Thomas
REGISTRATION NUMBER: 32,993
REFERENCE/DOCKET NUMBER: 135/1
TELECOMMUNICATION INFORMATION:

TELEPHONE: (919) 541-8614
TELEFAX: (919) 541-8689
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 560 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
IMMEDIATE SOURCE:
CLONE: 35S Promoter
US-09-291-238-5

Query Match 68.9%; Score 43.4; DB 4; Length 560;
Best Local Similarity 97.8%; Pred. No. 4.7e-09;
Matches 44; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 12 CTAAGTGGATTGATGATATCTCCACTGACGTAAGGATGACGCA 56
DB 316 CAAGTGGATTGATGATATCTCCACTGACGTAAGGATGACGCA 360

RESULT 14
US-09-330-760-5
Sequence 5, Application US/09330760
Patent No. 6229075
GENERAL INFORMATION:
APPLICANT: Irvin J. Mettler, Paul S. Dietrich, Ralph Sinibaldi
TITLE OF INVENTION: DNA Construct Containing Bacillus
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 6229075artis Corporation
STREET: 564 Morris Avenue
CITY: Summit
STATE: New Jersey
COUNTRY: USA
ZIP: 07901
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/330,760
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/042,426
FILING DATE: March 13, 1998
ATTORNEY/AGENT INFORMATION:
NAME: Hoxie, Thomas
REGISTRATION NUMBER: 32,993
REFERENCE/DOCKET NUMBER: 135/1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (919) 541-8614
TELEFAX: (919) 541-8689
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 560 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
IMMEDIATE SOURCE:
CLONE: 35S Promoter
US-09-330-760-5

Query Match 68.9%; Score 43.4; DB 4; Length 560;
Best Local Similarity 97.8%; Pred. No. 4.7e-09;


```
; Publication No. US20030028922A1
; GENERAL INFORMATION:
; APPLICANT: Meristem Therapeutics
; TITLE OF INVENTION: Chimeric expression promoters originating from commelina yellow
; TITLE OF INVENTION: virus and cassava vein mosaic virus
; FILE REFERENCE: 184332042
; CURRENT APPLICATION NUMBER: US/09/963,803
; CURRENT FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: FR 99/03925
; PRIOR FILING DATE: 1999-03-29
; PRIOR APPLICATION NUMBER: PCT IB00/00370
; PRIOR FILING DATE: 2000-10-05
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 7
; LENGTH: 301
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: promoter MP1154
; FEATURE:
; NAME/KEY: promoter
; LOCATION: (1)..(301)
; OTHER INFORMATION:
US-09-963-803-7
```

```
Query Match          93.7%; Score 59; DB 9; Length 301;
Best Local Similarity 100.0%; Pred. No. 2,1e-14;
Matches 59; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 5 CTCGACGACTAGTGGATTGATGTGATATCTCCACTGACGTAAGGATGACCATGCCACT 63
DB 13 CTCGACGACTAGTGGATTGATGTGATATCTCCACTGACGTAAGGATGACCATGCCACT 71
```

RESULT 3

```
US-09-963-803-6
; Sequence 6, Application US/09963803
; Publication No. US20030028922A1
; GENERAL INFORMATION:
; APPLICANT: Meristem Therapeutics
; TITLE OF INVENTION: Chimeric expression promoters originating from commelina yellow
; TITLE OF INVENTION: virus and cassava vein mosaic virus
; FILE REFERENCE: 184332042
; CURRENT APPLICATION NUMBER: US/09/963,803
; CURRENT FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: FR 99/03925
; PRIOR FILING DATE: 1999-03-29
; PRIOR APPLICATION NUMBER: PCT IB00/00370
; PRIOR FILING DATE: 2000-10-05
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
; LENGTH: 398
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: promoter MP1147
; FEATURE:
; NAME/KEY: promoter
; LOCATION: (1)..(398)
; OTHER INFORMATION:
US-09-963-803-6
```

```
Query Match          93.7%; Score 59; DB 9; Length 398;
Best Local Similarity 100.0%; Pred. No. 2,2e-14;
Matches 59; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 5 CTCGACGACTAGTGGATTGATGTGATATCTCCACTGACGTAAGGATGACCATGCCACT 63
DB 110 CTCGACGACTAGTGGATTGATGTGATATCTCCACTGACGTAAGGATGACCATGCCACT 168
```

```
RESULT 4
US-09-963-803-25
; Sequence 25, Application US/09963803
; Publication No. US20030028922A1
; GENERAL INFORMATION:
; APPLICANT: Meristem Therapeutics
; TITLE OF INVENTION: Chimeric expression promoters originating from commelina yellow
; TITLE OF INVENTION: virus and cassava vein mosaic virus
; FILE REFERENCE: 184332042
; CURRENT APPLICATION NUMBER: US/09/963,803
; CURRENT FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: FR 99/03925
; PRIOR FILING DATE: 1999-03-29
; PRIOR APPLICATION NUMBER: PCT IB00/00370
; PRIOR FILING DATE: 2000-10-05
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 25
; LENGTH: 472
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: promoter MP1169
; FEATURE:
; NAME/KEY: promoter
; LOCATION: (1)..(472)
; OTHER INFORMATION:
US-09-963-803-25
```

```
Query Match          93.7%; Score 59; DB 9; Length 472;
Best Local Similarity 100.0%; Pred. No. 2,4e-14;
Matches 59; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 5 CTCGACGACTAGTGGATTGATGTGATATCTCCACTGACGTAAGGATGACCATGCCACT 63
DB 110 CTCGACGACTAGTGGATTGATGTGATATCTCCACTGACGTAAGGATGACCATGCCACT 168
```

RESULT 5

```
US-09-963-803-24
; Sequence 24, Application US/09963803
; Publication No. US20030028922A1
; GENERAL INFORMATION:
; APPLICANT: Meristem Therapeutics
; TITLE OF INVENTION: Chimeric expression promoters originating from commelina yellow
; TITLE OF INVENTION: virus and cassava vein mosaic virus
; FILE REFERENCE: 184332042
; CURRENT APPLICATION NUMBER: US/09/963,803
; CURRENT FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: FR 99/03925
; PRIOR FILING DATE: 1999-03-29
; PRIOR APPLICATION NUMBER: PCT IB00/00370
; PRIOR FILING DATE: 2000-10-05
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 24
; LENGTH: 541
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: promoter MP1168
; FEATURE:
; NAME/KEY: promoter
; LOCATION: (1)..(541)
; OTHER INFORMATION:
US-09-963-803-24
```

```
Query Match          93.7%; Score 59; DB 9; Length 541;
Best Local Similarity 100.0%; Pred. No. 2,5e-14;
Matches 59; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 5 CTCGACGACTAGTGGATTGATGTGATATCTCCACTGACGTAAGGATGACCATGCCACT 63
DB 110 CTCGACGACTAGTGGATTGATGTGATATCTCCACTGACGTAAGGATGACCATGCCACT 168
```

Db 110 CTGCAGACTGATGATGTGATATCTCCACTGACGTAGGAGGATGACGATGCCACT 168

RESULT 6

US-09-963-803-23
Sequence 23, Application US/09963803
Publication No. US20030028922A1

GENERAL INFORMATION:

APPLICANT: Meristem Therapeutics
TITLE OF INVENTION: Chimeric expression promoters originating from commelina yellow m
TITLE OF INVENTION: virus and cassava vein mosaic virus

FILE REFERENCE: 184332042

CURRENT APPLICATION NUMBER: US/09/963,803

CURRENT FILING DATE: 2001-09-26

PRIOR APPLICATION NUMBER: FR 99/03925

PRIOR FILING DATE: 1999-03-29

PRIOR APPLICATION NUMBER: PCT IB00/00370

PRIOR FILING DATE: 2000-10-05

NUMBER OF SEQ ID NOS: 39

SOFTWARE: PatentIn version 3.1

SEQ ID NO 23

LENGTH: 604

TYPE: DNA

ORGANISM: Artificial Sequence

FEATURE:

NAME/KEY: promoter Mpr1167

LOCATION: (1)..(604)

OTHER INFORMATION:

US-09-963-803-23

Query Match

Best Local Similarity 93.7%; Score 59; DB 9; Length 604;

Matches 59; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

US-09-963-803-14

Sequence 14, Application US/09963803

Publication No. US20030028922A1

GENERAL INFORMATION:

APPLICANT: Meristem Therapeutics

TITLE OF INVENTION: Chimeric expression promoters originating from commelina yellow m

TITLE OF INVENTION: virus and cassava vein mosaic virus

FILE REFERENCE: 184332042

CURRENT APPLICATION NUMBER: US/09/963,803

CURRENT FILING DATE: 2001-09-26

PRIOR APPLICATION NUMBER: FR 99/03925

PRIOR FILING DATE: 1999-03-29

PRIOR APPLICATION NUMBER: PCT IB00/00370

PRIOR FILING DATE: 2000-10-05

NUMBER OF SEQ ID NOS: 39

SOFTWARE: PatentIn version 3.1

SEQ ID NO 14

LENGTH: 79

TYPE: DNA

ORGANISM: Artificial Sequence

FEATURE:

NAME/KEY: promoter Mpr1164

LOCATION: (1)..(392)

OTHER INFORMATION:

US-09-963-803-14

Query Match

Best Local Similarity 73.0%; Score 46; DB 9; Length 79;

Matches 46; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

US-09-963-803-21

Sequence 21, Application US/09963803

Publication No. US20030028922A1

GENERAL INFORMATION:

APPLICANT: Meristem Therapeutics

TITLE OF INVENTION: Chimeric expression promoters originating from commelina yellow m

TITLE OF INVENTION: virus and cassava vein mosaic virus

FILE REFERENCE: 184332042

CURRENT APPLICATION NUMBER: US/09/963,803

CURRENT FILING DATE: 2001-09-26

PRIOR APPLICATION NUMBER: FR 99/03925

PRIOR FILING DATE: 1999-03-29

PRIOR APPLICATION NUMBER: PCT IB00/00370

PRIOR FILING DATE: 2000-10-05

NUMBER OF SEQ ID NOS: 39

SOFTWARE: PatentIn version 3.1

SEQ ID NO 21

LENGTH: 392

TYPE: DNA

ORGANISM: Artificial Sequence

FEATURE:

NAME/KEY: promoter Mpr1164

LOCATION: (1)..(392)

OTHER INFORMATION:

US-09-963-803-21

Query Match

Best Local Similarity 71.4%; Score 45; DB 9; Length 392;

Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 34 GATTGATGTATCTCCACTGACGTAGGAGGATGACGATGCCACT 79

RESULT 8

US-09-963-803-5
Sequence 5, Application US/09963803
Publication No. US20030028922A1

GENERAL INFORMATION:

APPLICANT: Meristem Therapeutics
TITLE OF INVENTION: Chimeric expression promoters originating from commelina yellow m
TITLE OF INVENTION: virus and cassava vein mosaic virus

FILE REFERENCE: 184332042

CURRENT APPLICATION NUMBER: US/09/963,803

CURRENT FILING DATE: 2001-09-26

PRIOR APPLICATION NUMBER: FR 99/03925

PRIOR FILING DATE: 1999-03-29

PRIOR APPLICATION NUMBER: PCT IB00/00370

PRIOR FILING DATE: 2000-10-05

NUMBER OF SEQ ID NOS: 39

SOFTWARE: PatentIn version 3.1

SEQ ID NO 5

LENGTH: 371

TYPE: DNA

ORGANISM: Artificial Sequence

FEATURE:

NAME/KEY: promoter Mpr1146

LOCATION: (1)..(371)

OTHER INFORMATION:

US-09-963-803-5

Query Match

Best Local Similarity 73.0%; Score 46; DB 9; Length 371;

Matches 46; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

US-09-963-803-21/c

Sequence 21, Application US/09963803

Publication No. US20030028922A1

GENERAL INFORMATION:

APPLICANT: Meristem Therapeutics

TITLE OF INVENTION: Chimeric expression promoters originating from commelina yellow m

TITLE OF INVENTION: virus and cassava vein mosaic virus

FILE REFERENCE: 184332042

CURRENT APPLICATION NUMBER: US/09/963,803

CURRENT FILING DATE: 2001-09-26

PRIOR APPLICATION NUMBER: FR 99/03925

PRIOR FILING DATE: 1999-03-29

PRIOR APPLICATION NUMBER: PCT IB00/00370

PRIOR FILING DATE: 2000-10-05

NUMBER OF SEQ ID NOS: 39

SOFTWARE: PatentIn version 3.1

SEQ ID NO 21

LENGTH: 392

TYPE: DNA

ORGANISM: Artificial Sequence

FEATURE:

NAME/KEY: promoter Mpr1164

LOCATION: (1)..(392)

OTHER INFORMATION:

US-09-963-803-21

Query Match

Best Local Similarity 71.4%; Score 45; DB 9; Length 392;

Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 18 GATTGATGATATCTCCACTGACGTAAAGGATGACGATGCCAC 62
|||||
Db 278 GATTGATGATATCTCCACTGACGTAAAGGATGACGATGCCAC 234

RESULT 10
US-09-963-803-19

; Sequence 19, Application US/09963803
; Publication No. US20030028922A1
; GENERAL INFORMATION:

; APPLICANT: Meristem Therapeutics
; TITLE OF INVENTION: Chimeric expression promoters originating from commelina yellow
; FILE REFERENCE: 184332042
; CURRENT APPLICATION NUMBER: US/09/963,803
; PRIOR FILING DATE: 2001-09-26

; PRIOR APPLICATION NUMBER: FR 99/03925
; PRIOR FILING DATE: 1999-03-29
; PRIOR APPLICATION NUMBER: PCT IB00/00370
; PRIOR FILING DATE: 2000-10-05

; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 19

; LENGTH: 393
; TYPE: DNA

; ORGANISM: Artificial Sequence
; FEATURE:

; OTHER INFORMATION: promoter MPr1162
; FEATURE:

; NAME/KEY: promoter
; LOCATION: (1)..(393)

; OTHER INFORMATION:
US-09-963-803-19

Query Match

71.4%; Score 45; DB 9; Length 393;

Best Local Similarity 100.0%; Pred. No. 1.2e-08; Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 18 GATTGATGATATCTCCACTGACGTAAAGGATGACGATGCCAC 62
|||||
Db 258 GATTGATGATATCTCCACTGACGTAAAGGATGACGATGCCAC 302

RESULT 11
US-09-963-803-20

; Sequence 20, Application US/09963803
; Publication No. US20030028922A1
; GENERAL INFORMATION:

; APPLICANT: Meristem Therapeutics
; TITLE OF INVENTION: Chimeric expression promoters originating from commelina yellow
; FILE REFERENCE: 184332042
; CURRENT APPLICATION NUMBER: US/09/963,803
; PRIOR FILING DATE: 2001-09-26

; PRIOR APPLICATION NUMBER: FR 99/03925
; PRIOR FILING DATE: 1999-03-29
; PRIOR APPLICATION NUMBER: PCT IB00/00370
; PRIOR FILING DATE: 2000-10-05

; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 20

; LENGTH: 462
; TYPE: DNA

; ORGANISM: Artificial Sequence
; FEATURE:

; OTHER INFORMATION: promoter MPr1163
; FEATURE:

; NAME/KEY: promoter
; LOCATION: (1)..(462)

; OTHER INFORMATION:
US-09-963-803-20

Query Match 71.4%; Score 45; DB 9; Length 462;
Best Local Similarity 100.0%; Pred. No. 1.2e-08; Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 18 GATTGATGATATCTCCACTGACGTAAAGGATGACGATGCCAC 62
|||||
Db 258 GATTGATGATATCTCCACTGACGTAAAGGATGACGATGCCAC 302

RESULT 12
US-09-963-803-22

; Sequence 22, Application US/09963803
; Publication No. US20030028922A1
; GENERAL INFORMATION:

; APPLICANT: Meristem Therapeutics
; TITLE OF INVENTION: Chimeric expression promoters originating from commelina yellow
; FILE REFERENCE: 184332042
; CURRENT APPLICATION NUMBER: US/09/963,803
; PRIOR FILING DATE: 2001-09-26

; PRIOR APPLICATION NUMBER: FR 99/03925
; PRIOR FILING DATE: 1999-03-29
; PRIOR APPLICATION NUMBER: PCT IB00/00370
; PRIOR FILING DATE: 2000-10-05

; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 22

; LENGTH: 600
; TYPE: DNA

; ORGANISM: Artificial Sequence
; FEATURE:

; OTHER INFORMATION: promoter MPr1165
; FEATURE:

; NAME/KEY: promoter
; LOCATION: (1)..(600)

; OTHER INFORMATION:
US-09-963-803-22

Query Match

71.4%; Score 45; DB 9; Length 600;

Best Local Similarity 100.0%; Pred. No. 1.3e-08; Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 18 GATTGATGATATCTCCACTGACGTAAAGGATGACGATGCCAC 62
|||||
Db 396 GATTGATGATATCTCCACTGACGTAAAGGATGACGATGCCAC 440

RESULT 13
US-10-012-070A-47

; Sequence 47, Application US/10012070A
; Publication No. US20030077801A1
; GENERAL INFORMATION:

; APPLICANT: Hawkes, Timothy
; APPLICANT: Warner, Simon
; APPLICANT: Bachoo, Satyinder
; APPLICANT: Pickerill, Andrew

; TITLE OF INVENTION: Herbicide Resistant Plants
; FILE REFERENCE: 50490/UST
; CURRENT APPLICATION NUMBER: US/10/012,070A
; PRIOR FILING DATE: 2001-10-29

; PRIOR APPLICATION NUMBER: PCT/GB00/01573
; PRIOR FILING DATE: 2000-04-20
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 47
; LENGTH: 309

; TYPE: DNA

; ORGANISM: Cauliflower mosaic virus
US-10-012-070A-47

Query Match

68.9%; Score 43.4; DB 9; Length 309;

Best Local Similarity 97.8%; Pred. No. 4.9e-08;

	Matches	44,	Conservative	0;	Mismatches	1;	Indels	0;	Gaps	0;
Qy	12	CTAGTGGATTGATGTGATATCTCCACTGACCGTAAGGATGACCA	56	I						
Dd	236	CAGTGGAATTGATGTGATATCTCCACTGACCGTAAGGATGACCA	280							

Search completed: May 24, 2003, 15:36:02
Job time : 50.1129 secs

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RESULT 14
US-09-951-470-3
: Sequence 3, Application US/09951470
: Patent No. US20020102582A1
: GENERAL INFORMATION:
: APPLICANT: Levine, Elaine
: TITLE OF INVENTION: Corn Event MON 810 and Compositions and Methods for Detection The
: FILE REFERENCE: 38-21 (52220)B
: CURRENT APPLICATION NUMBER: US/09/951,470
: PRIORITY FILING DATE: 2001-09-13
: PRIOR APPLICATION NUMBER: 60/232,208
: PRIOR FILING DATE: 2000-09-13
: NUMBER OF SEQ ID NOS: 10
: SOFTWARE: PatentIn version 3.0
: SEQ ID NO 3
: LENGTH: 566
: TYPE: DNA
: ORGANISM: corn
: FEATURE:
: NAME/KEY: DNA
: LOCATION: (1) ..(566)
: OTHER INFORMATION: 5' genome+insert sequence
US-09-951-470-3

```

Query Match	68.9%;	Score 43.4;	DB 10;	Length 566;
Best Local Similarity	97.8%;	Pred. NO. 5.9e-08;		
Matches 44;	Conservative	0;	Mismatches 1;	Indels 0;
				Gaps 0;

OY 12 CTAGTGGATTGATGTGATATCTCCACTGACGTAAGGATGACGCA 56
 | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 435 CAAGTGATTGATGTGATATCTCCACTGACGTAAGGATGACGCA 479

RESULT 15
 US-09-943-692-33
 Sequence 33, Application US/09943692
 Patent No. US20020152496A1
 GENERAL INFORMATION:
 APPLICANT: FISCHHOFF, DAVID A.
 APPLICANT: FUCHS, ROY L.
 APPLICANT: LAVRIK, PAUL B.
 APPLICANT: MCPHERSON, SYLVIA A.
 APPLICANT: PERLAK, FREDERICK J.
 TITLE OF INVENTION: COLEOPTERAN TOXIN PROTEINS OF BACILLUS THURINGIENSIS
 FILE REFERENCE: MOBP-195-1
 CURRENT APPLICATION NUMBER: US/09/943,692
 CURRENT FILING DATE: 2001-08-31
 PRIOR APPLICATION NUMBER: 09/027,998
 PRIOR FILING DATE: 1998-02-23
 NUMBER OF SEQ ID NOS: 54
 SOFTWARE: PatentIn version 3.1
 SEQ ID NO 33
 LENGTH: 661
 TYPE: DNA
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: Recombinant Cauliflower Mosaic Viral Promoter (CAMV35S)
 US-09-943-692-33

Query Match	68.9%	Score 43.4;	DB 10;	Length 661;
Best Local Similarity	97.8%;	Pred. No. 6.1e-08;		
Matches 44;	Conservative 0;	Mismatches 1;	Indels 0;	Gaps 0;

QY	12	CTAGTGGA	TTGATGTG	ATATCTCC	ACTGAC	GTAA	GGGATG	ACGCA	56
	1								
Db	524	CAAGTGGA	TTGATGTG <td>ATATCTCC <td>ACTGAC <td>GTAA <td>GGGATG <td>ACGCA</td> <td>568</td> </td></td></td></td>	ATATCTCC <td>ACTGAC <td>GTAA <td>GGGATG <td>ACGCA</td> <td>568</td> </td></td></td>	ACTGAC <td>GTAA <td>GGGATG <td>ACGCA</td> <td>568</td> </td></td>	GTAA <td>GGGATG <td>ACGCA</td> <td>568</td> </td>	GGGATG <td>ACGCA</td> <td>568</td>	ACGCA	568


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FEATURES
source
    Class: TDNA tagged.
    Location/Qualifiers
        1..193
            /organism="Arabidopsis thaliana"
            /strain="Columbia 0"
            /db_xref="taxon:3702"
            /clone="SAIK_045097.54.25.x"
            /clone_lib="Arabidopsis thaliana TDNA insertion lines"
            /note="PCR was performed on Arabidopsis thaliana lines each of which contains one or more TDNA insertion elements. The resultant fragment for each line was directly sequenced to determine the genomic sequence at the site of insertion. Details of the protocols used can be found at http://signal.salk.edu/cdna_protocols.html"

BASE COUNT
61 a      48 c      43 g      41 t

ORIGIN
Query Match          71.1%; Score 44.8; DB 17; Length 193;
Best Local Similarity 87.5%; Pred. NO. 1.5e-05;
Matches 49; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Oy   1 CATGTCGCAGACTAGTGGATTGATGTGATCATCTCCACGTACGCTAAGGATGACGA 56
     ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db   67 CATCTCAAGCAAGCAAGTGATTCATGATGTGATTCATCTCCACGTACGCTAAGGATGACGA 122

RESULT 2
LOCUS       BH747756                      405 bp    DNA         linear    GSS 27-FEB-2002
DEFINITION  Arabidopsis thaliana genome clone SALK_033959.47.55.x, DNA sequence.
VERSION     BH747756
KEYWORDS    GSS.

ORGANISM    Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsi.
1 (bases 1 to 405)
Alonso,J.M., Leisner,T.J., Barajas,P., Chen,H., Cheuk,R., Gadgilab,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L., Shinn,P., Zimmermann,J. and Ecker,J.R.
A Sequence Indexed Library of Insertion Mutations in the Arabidopsis Genome
Contact: Joseph R. Ecker
Salk Institute Genomic Analysis Laboratory (Signal)
The Salk Institute for Biological Studies
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
Tel.: 858 453 4100 x1752
Fax: 858 558 6379
Email: eckers@salk.edu
This is single pass sequence recovered from the left border of TDNA.
Class: TDNA tagged.
Location/Qualifiers
    1..405
        /organism="Arabidopsis thaliana"
        /strain="Columbia 0"
        /db_xref="taxon:3702"
        /clone="SAIK_033959.47.55.x"
        /clone_lib="Arabidopsis thaliana TDNA insertion lines"
        /note="PCR was performed on Arabidopsis thaliana lines each of which contains one or more TDNA insertion elements. The resultant fragment for each line was directly sequenced to determine the genomic sequence at the site of insertion. Details of the protocols used can be found at http://signal.salk.edu/cdna_protocols.html"

BASE COUNT
105 a      109 c      105 g      86 t

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Query Match	69.5%	Score 43.8	DB 17	Length 405
Best Local Similarity	95.7%	Pred. No. 4.5e-05		
Matches 45	Conservative 0	Mismatches 2	Indels 0	Gaps 0
QY	10	GACATAGTGGATTGATATCTCCACTGACGTAAGGATGACGCA	56	
Db	288	GGCAAGTGGATTGATATCTCCACTGACGTAAGGATGACGCA	334	
RESULT 3				
LOCUS	BH749349			
DEFINITION	BH749349	142 bp	DNA	linear GSS 27-FEB-2002
SOURCE	Arabidopsis thaliana genomic clone	SALK_047736.48.15.x	DNA	
ACCESSION	BH749349			
VERSION	BH749349.1	GI:18964144		
KEYWORDS	GSS.			
ORGANISM	thale cress.			
REFERENCE	Alonso,J.M., Leisner,T.J., Barrajas,P., Chen,H., Cheuk,R., Gadrinab ,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L., Shinn,P., Zimmerman,J. and Ecker,J.R.			
AUTHORS	A Sequence-Indexed Library of Insertion Mutations in the Arabidopsis Genome			
TITLE	Unpublished (2001)			
JOURNAL	Contact: Joseph R. Ecker			
COMMENT	Salk Institute Genomic Analysis Laboratory (SIGNAL)			
	The Salk Institute for Biological Studies			
	10010 N. Torrey Pines Road, La Jolla, CA 92037, USA			
	Tel: 858 453 4100 x1752			
	Fax: 858 558 6379			
	Email: eckers@salk.edu			
	This is single pass sequence recovered from the left border of TDNA.			
FEATURES	Class: TDNA tagged.			
SOURCE	Location/Qualifiers			
	1..142			
	/organism="Arabidopsis thaliana"			
	/strain="Columbia 0"			
	/db.xref="taxon:3702"			
	/clone="SALK_047736.48.15.x"			
	/clone_lib="Arabidopsis thaliana TDNA insertion lines"			
	/note="PCR was performed on Arabidopsis thaliana lines each of which contains one or more TDNA insertion elements. The resultant fragment for each line was directly sequenced to determine the genomic sequence at the site of insertion. Details of the protocols used can be found at http://signal.salk.edu/cdna_protocols.html "			
BASE COUNT	41 a	36 c	30 g	35 t
ORIGIN				
Query Match	68.9%	Score 43.4	DB 17	Length 142
Best Local Similarity	97.8%	Pred. No. 4e-05		
Matches 44	Conservative 0	Mismatches 1	Indels 0	Gaps 0
QY	12	CTAGTGGATTGATATCTCCACTGACGTAAGGATGACGCA	56	
Db	27	CAAGTGATGTGATGATATCTCCACTGACGTAAGGATGACGCA	71	
RESULT 4				
LOCUS	BH619283	153 bp	DNA	linear GSS 30-JAN-2002
DEFINITION	SALK_040762 Arabidopsis thaliana TDNA insertion lines			
SOURCE	thaliana genomic clone SALK_040762, DNA sequence.			
ACCESSION	BH619283			
VERSION	BH619283.1	GI:18429799		

[illegible]

```

Tel: 858 453 4100 x1752
Fax: 858 558 6379
Email: eckeresalk.edu
This is single pass sequence recovered from the left border of
TDNA.
Class: TDNA tagged.

FEATURES
Source
Location/Qualifiers
1..153
/organism="Arabidopsis thaliana"
/strain="Columbia 0"
/db_xref="taxon:3702"
/clone="SALK_008070.43.05.x"
/clone_lib="Arabidopsis thaliana TDNA insertion lines"
/note="PCR was performed on Arabidopsis thaliana lines
each of which contains one or more TDNA insertion
elements. The resultant fragment for each line was
directly sequenced to determine the genomic sequence at
the site of insertion. Details of the protocols used can
be found at http://signal.salk.edu/cdna\_protocols.html"

BASE COUNT
47 a 37 c 33 g 36 t

ORIGIN
Query Match 68.9%; Score 43.4; DB 17; Length 153;
Best Local Similarity 97.8%; Pred. No. 4.2e-05;
Matches 44; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Df 12 CTAGTGATGTGATGTGATATCTCCACGTGACGTAGGATGACGA 56
1 |||||||||||||||||||||||||||||||||||||||
38 CAAGTGATGTGATGTGATATCTCCACGTGACGTAGGATGACGA 82

RESULT 6
BH748291/c 158 bp DNA linear GSS 27-FEB-2002
LOCUS SALK_045100.51.10.x Arabidopsis thaliana TDNA insertion lines
DEFINITION Arabidopsis thaliana genomic clone SALK_045100.51.10.x, DNA
sequence.
ACCESSION BH748291
VERSION BH748291
KEYWORDS GI:18961648
SOURCE thale cress.
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
1 (bases 1 to 158)
Alonso,J.M., Leisner,T.J., Barajas,P., Chen,H., Cheuk,R., Gadgilnab
,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L., Shinn,P.,
Zimmerman,J. and Ecker,J.R.
A Sequence-Indexed Library of Insertion Mutations in the
Arabidopsis Genome
Contact: Joseph R. Ecker
Unpublished (2001)
The Salk Institute Genomic Analysis Laboratory (SIGNAL)
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
Tel: 858 453 4100 x1752
Fax: 858 558 6379
Email: eckeresalk.edu
This is single pass sequence recovered from the left border of
TDNA.
Class: TDNA tagged.
Location/Qualifiers
1..158
/organism="Arabidopsis thaliana"
/strain="Columbia 0"
/db_xref="taxon:3702"
/clone="SALK_045100.51.10.x"
/clone_lib="Arabidopsis thaliana TDNA insertion lines"
/note="PCR was performed on Arabidopsis thaliana lines
each of which contains one or more TDNA insertion
elements. The resultant fragment for each line was
directly sequenced to determine the genomic sequence at

```


JOURNAL
COMMENT

Unpublished (2001)
Contact: Joseph R. Ecker
Salk Institute Genomic Analysis Laboratory (Signal)
The Salk Institute for Biological Studies
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
Tel: 858 453 4100 x1752
Fax: 858 558 6379
Email: eckersalk.edu

This is single pass sequence recovered from the left border of TDNA.

FEATURES

source
Class: TDNA tagged.
Location/Qualifiers

1. .190

/organism="Arabidopsis thaliana"

/strain="Columbia 0"

/db_xref="taxon:3702"

/clone_lib="Arabidopsis thaliana TDNA insertion lines"

/note="PCR was performed on Arabidopsis thaliana lines each of which contains one or more TDNA insertion elements. The resultant fragment for each line was directly sequenced to determine the genomic sequence at the site of insertion. Details of the protocols used can be found at http://signal.salk.edu/tdna_protocols.html"

BASE COUNT

52 a 52 c 41 g 45 t

ORIGIN

Query Match

Best Local Similarity 97.8%; Score 43.4; DB 17; Length 190;

Matches 44; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY

12 CTAGTGATGATGATGATCTCCACTGACGTAAGGATGACGCA 56

75 CAAGTGATGATGATGATCTCCACTGACGTAAGGATGACGCA 119

RESULT 10
BH747829
LOCUS

BH747829 214 bp DNA linear GSS 27-FEB-2002
SALK_035354.55.75.x Arabidopsis thaliana TDNA insertion lines
Arabidopsis thaliana genomic clone SALK_035354.55.75.x, DNA sequence.

ACCESSION

BH747829

VERSION

BH747829.1 GI:18960944

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
1 (bases 1 to 214)
Alonso, J.M., Leisner, T.J., Barajas, P., Chen, H., Cheuk, R., Gadrinab, C., Jeske, A., Karnes, M., Kim, C.J., Parker, H., Prednis, L., Shinn, P., Zimmerman, J., and Ecker, J.R.
A Sequence-Indexed Library of Insertion Mutations in the Arabidopsis Genome
Unpublished (2001)
Contact: Joseph R. Ecker
Salk Institute Genomic Analysis Laboratory (Signal)
The Salk Institute for Biological Studies
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
Tel: 858 453 4100 x1752
Fax: 858 558 6379
Email: eckersalk.edu
This is single pass sequence recovered from the left border of TDNA.

Class: TDNA tagged.

Location/Qualifiers

1. .214

/organism="Arabidopsis thaliana"

/strain="Columbia 0"

/db_xref="taxon:3702"

/clone="SALK_035354.55.75.x"

/clone_lib="Arabidopsis thaliana TDNA insertion lines"

/note="PCR was performed on Arabidopsis thaliana lines each of which contains one or more TDNA insertion elements. The resultant fragment for each line was directly sequenced to determine the genomic sequence at the site of insertion. Details of the protocols used can be found at http://signal.salk.edu/tdna_protocols.html"

BASE COUNT

58 a 56 c 52 g 48 t

ORIGIN

Query Match

Best Local Similarity 97.8%; Score 43.4; DB 17; Length 214;

Matches 44; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY

12 CTAGTGATGATGATGATCTCCACTGACGTAAGGATGACGCA 56

98 CAAGTGATGATGATGATCTCCACTGACGTAAGGATGACGCA 142

RESULT 11
BH753813
LOCUS

BH753813 215 bp DNA linear GSS 27-FEB-2002
SALK_029677.55.00.x Arabidopsis thaliana TDNA insertion lines
Arabidopsis thaliana genomic clone SALK_029677.55.00.x, DNA sequence.

ACCESSION

BH753813

VERSION

BH753813.1 GI:18974308

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
1 (bases 1 to 215)
Alonso, J.M., Leisner, T.J., Barajas, P., Chen, H., Cheuk, R., Gadrinab, C., Jeske, A., Karnes, M., Kim, C.J., Parker, H., Prednis, L., Shinn, P., Zimmerman, J., and Ecker, J.R.
A Sequence-Indexed Library of Insertion Mutations in the Arabidopsis Genome
Unpublished (2001)
Contact: Joseph R. Ecker
Salk Institute Genomic Analysis Laboratory (Signal)
The Salk Institute for Biological Studies
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
Tel: 858 453 4100 x1752
Fax: 858 558 6379
Email: eckersalk.edu
This is single pass sequence recovered from the left border of TDNA.

Class: TDNA tagged.

Location/Qualifiers

1. .215

/organism="Arabidopsis thaliana"

/strain="Columbia 0"

/db_xref="taxon:3702"

/clone="SALK_029677.55.00.x"

/note="PCR was performed on Arabidopsis thaliana lines each of which contains one or more TDNA insertion elements. The resultant fragment for each line was directly sequenced to determine the genomic sequence at the site of insertion. Details of the protocols used can be found at http://signal.salk.edu/tdna_protocols.html"

63 a 56 c 50 g 46 t

BASE COUNT

ORIGIN

Query Match

Best Local Similarity 97.8%; Score 43.4; DB 17; Length 215;

Matches 44; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY

12 CTAGTGATGATGATGATCTCCACTGACGTAAGGATGACGCA 56

99 CAAGTGATGATGATGATCTCCACTGACGTAAGGATGACGCA 143

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DEFINITION	SAIK_033710.53.75.x Arabidopsis thaliana TDNA insertion lines
ACCESSION	BH747744
VERSION	BH747744
KEYWORDS	GSS.
ORGANISM	thale cress.
REFERENCE	Alonso,J.M., Lejane,T.J., Barajas,P., Chen,H., Cheuk,R., Godfrinab ,C., Jeske,A., Karnes,H., Kim,C.J., Parker,H., Prednis,L., Shinn,P., Zimmerman,J. and Ecker,J.R.
AUTHORS	A Sequence-Indexed Library of Insertion Mutations in the Arabidopsis genome Unpublished (2001)
JOURNAL	Contact: Joseph R. Ecker
COMMENT	Salk Institute Genomic Analysis Laboratory (SIGAL) The Salk Institute for Biological Studies 10010 N. Torrey Pines Road, La Jolla, CA 92037, USA Tel.: 858 453 4100 x1752 Fax: 858 558 6379 Email: eckeresalk.edu This is single pass sequence recovered from the left border of TDNA.
FEATURES	Class: TDNA tagged.
source	Location/Qualifiers
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	/strain="Columbia 0"
	/db_xref="taxon:3702"
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	/clone_11b="Arabidopsis thaliana TDNA insertion lines"
	/note="PCR was performed on Arabidopsis thaliana lines each of which contains one or more TDNA insertion elements. The resultant fragment for each line was directly sequenced to determine the genomic sequence at the site of insertion. Details of the protocols used can be found at http://signal.salk.edu/cdna_protocols.html "
BASE COUNT	66 a 57 c 50 g 46 t
ORIGIN	
Query Match	68.9%; Score 43.4; DB 17; Length 219;
Best Local Similarity	97.8%; Pred. No. 4.8e-05;
Matches	44: Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY	12 CAGTCGATGATGATGATATCTCCACTGACGTAAGGATGACGCA 56
Db	103 CAGTCGATGATGATGATATCTCCACTGACGTAAGGATGACGCA 147
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LOCUS	BH747438 220 bp DNA linear GSS 27-FEB-2002
DEFINITION	SAIK_017469.51.60.x Arabidopsis thaliana TDNA insertion lines
ACCESSION	BH747438
VERSION	BH747438
KEYWORDS	GSS.
ORGANISM	thale cress.
REFERENCE	Alonso,J.M., Lejane,T.J., Barajas,P., Chen,H., Cheuk,R., Godfrinab ,C., Jeske,A., Karnes,H., Kim,C.J., Parker,H., Prednis,L., Shinn,P., Zimmerman,J. and Ecker,J.R.
AUTHORS	A Sequence-Indexed Library of Insertion Mutations in the Arabidopsis genome Unpublished (2001)
JOURNAL	Contact: Joseph R. Ecker
COMMENT	Salk Institute Genomic Analysis Laboratory (SIGAL) The Salk Institute for Biological Studies 10010 N. Torrey Pines Road, La Jolla, CA 92037, USA Tel.: 858 453 4100 x1752 Fax: 858 558 6379 Email: eckeresalk.edu This is single pass sequence recovered from the left border of TDNA.
FEATURES	Class: TDNA tagged.
source	Location/Qualifiers
	1..219
	/organism="Arabidopsis thaliana"
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	/db_xref="taxon:3702"
	/clone="SAIK_033710.53.75.x"
	/clone_11b="Arabidopsis thaliana TDNA insertion lines"
	/note="PCR was performed on Arabidopsis thaliana lines each of which contains one or more TDNA insertion elements. The resultant fragment for each line was directly sequenced to determine the genomic sequence at the site of insertion. Details of the protocols used can be found at http://signal.salk.edu/cdna_protocols.html "
BASE COUNT	66 a 57 c 50 g 46 t
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Query Match	68.9%; Score 43.4; DB 17; Length 219;
Best Local Similarity	97.8%; Pred. No. 4.8e-05;
Matches	44: Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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LOCUS	BH746474
DEFINITION	BH746474 230 bp DNA linear GSS 27-FEB-2007
ACCESSION	SAIK_042817.55.00.x Arabidopsis thaliana TMA insertion lines
VERSION	Arabidopsis thaliana genomic clone SAIK_042817.55.00.x, DNA sequence.
KEYWORDS	BH746474 BH746474 GI:18939589
SOURCE	GSS.
ORGANISM	thale cress. Arabidopsis thaliana Arabidopsis thaliana

REFERENCE
Alonso, J.M., Leissle, T.J., Barajas, P., Chen, H., Cheuk, R., Gadgilnab
AUTHORS 'C., Jeske, A., Karnes, M., Kim, C.J., Parker, H., Prednais, L., Shinn, P
TITLE Zimmerman, J. and Ecker, J.R.
A Sequence-Indexed Library of Insertion Mutations in the
JOURNAL Arabidopsis Genome
COMMENT Unpublished (2001)
Contact: Joseph R. Ecker

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Class: TDNA tagged.
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each of which contains one or more TDNA insertion
elements. The resultant fragment for each line was
directly sequenced to determine the genomic sequence at
the site of insertion. Details of the protocols used can
be found at http://signal.salk.edu/cdna\_protocols.html"
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Db      115 CAAAGGATGTGATGTGATATCTCCACTGACGTAAAGGATGACGCA 159

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Job time : 829.806 secs

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GenCore version 5.1.4.p5.4578
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OM nucleic - nucleic search, using sw model

Run on: May 24, 2003, 10:21:51 ; Search time 334.194 Seconds

(without alignments)
5225.021 Million cell updates/sec

Title: US-09-963-803-9

Perfect score: 60
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Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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2: gb_hlg.*
3: gb_in.*
4: gb_om.*
5: gb_ov.*
6: gb_pat.*
7: gb_ph.*
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9: gb_pr.*
10: gb_ro.*
11: gb_sts.*
12: gb_sy.*
13: gb_un.*
14: gb_vl.*
15: em_da.*
16: em_fun.*
17: em_hum.*
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19: em_lnu.*
20: em_om.*
21: em_or.*
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23: em_pat.*
24: em_ph.*
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26: em_ro.*
27: em_sts.*
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29: em_vl.*
30: em_hlg_hum.*
31: em_hlg_in.*
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34: em_hlg_pln.*
35: em_hlg_rtd.*
36: em_hlg_mam.*
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40: em_hlggo_mus.*
41: em_hlggo_other.*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	60	100.0	60	6	AX036743 Sequence
2	60	100.0	317	6	AX036737 Sequence
3	60	100.0	348	6	AX036738 Sequence
4	60	100.0	392	6	AX036753 Sequence
5	60	100.0	393	6	AX036755 Sequence
6	60	100.0	462	6	AX036754 Sequence
7	60	100.0	600	6	AX036756 Sequence
8	60	100.0	9285	6	AX093047 Sequence
9	60	100.0	15077	6	AX093052 Sequence
10	55.4	92.3	301	6	AX036741 Sequence
11	55.4	92.3	371	6	AX036739 Sequence
12	55.4	92.3	398	6	AX036740 Sequence
13	55.4	92.3	472	6	AX036759 Sequence
14	55.4	92.3	541	6	AX036758 Sequence
15	55.4	92.3	604	6	AX036757 Sequence
16	40.4	67.3	515	6	AX036736 Sequence
17	40.4	67.3	516	6	AX088388 Sequence
18	40.4	67.3	532	6	AX020213 Sequence
19	40.4	67.3	593	6	AX088390 Sequence
20	40.4	67.3	838	6	AX014764 Sequence
21	40.4	67.3	853	6	AX088389 Sequence
22	40.4	67.3	857	6	AX088391 Sequence
23	40.4	67.3	931	6	AX088392 Sequence
24	40.4	67.3	931	6	AX088393 Sequence
25	40.4	67.3	1036	6	AX014765 Sequence
26	40.4	67.3	8158	14	CYU20341
27	40.4	67.3	8159	14	CYU58751
28	40.4	67.3	8340	6	AX329231
29	40.4	67.3	8340	6	AX338536 Sequence
30	40.4	67.3	12241	6	AX412168 Sequence
31	40.4	67.3	12241	6	AX412168 Sequence
32	27.6	46.0	43649	2	AC120006 Mus muscu
33	27.6	46.0	167852	2	AC072061 Homo sapi
34	27.6	46.0	176454	2	AC111873 Rattus no
35	27.6	46.0	177876	2	AC124942 Rattus no
36	27.6	46.0	227160	2	AC095908 Rattus no
37	27.2	45.3	177648	2	AC011323 Homo sapi
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39	27.2	45.3	198468	9	AC098477 Homo sapi
40	27.2	45.3	237560	2	AL845481 Dario ter
41	27	45.0	11953	9	AL646019 Human DNA
42	27	45.0	179694	2	AC115910 Mus muscu
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ALIGNMENTS

RESULT 1
AX036743 LOCUS AX036743 60 bp DNA linear PAT 16-NOV-2000
DEFINITION Sequence 9 from Patent WO0058485.
ACCESSION AX036743
VERSION AX036743.1 GI:11226252
KEYWORDS
SOURCE
ORGANISM
synthetic construct.
synthetic construct.
artificial sequences.
REFERENCE
1 (bases 1 to 60)
Rance, I., Theisen, M. and Gruber, V.
Chimeric expression promoters originating from commelina yellow
mottle virus and cassava vein mosaic virus
JOURNAL Patent: WO 0058485-A 9 05-OCT-2000;

MERISTEM THERAPEUTICS (FR) ; RANCE IANN (FR) ; THEISEN MANFRED (FR)
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/organism="synthetic construct"
/db_xref="taxon:32630"
/note="Directional desoxynucleotide building block 52"

BASE COUNT 25 a 12 c 13 g 10 t

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Matches 60; Conservative 0; Mismatches 0;

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Db 1 AGCCATGACACTCTGTGCGAATATTGAAGACGTGAAGCAGTGCAGCAACAATGAAAGAA 60

RESULT 2
AX036737
LOCUS AX036737 317 bp DNA linear PAT 16-NOV-2000
DEFINITION Sequence 3 from Patent WO0058485.
ACCESSION AX036737
VERSION AX036737.1 GI:11226246
KEYWORDS
SOURCE synthetic construct.
ORGANISM synthetic construct.
REFERENCE 1 (bases 1 to 317)
AUTHORS Rance, I., Theisen, M., and Gruber, V.
TITLE ChimERIC expression promoters originating from commelina yellow
mottle virus and cassava vein mosaic virus
Patent: WO 0058485-A 3 05-OCT-2000;
JOURNAL MERISTEM THERAPEUTICS (FR) ; RANCE IANN (FR) ; THEISEN MANFRED (FR)

FEATURES
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/db_xref="taxon:32630"
/note="promoter Mp1116"

Promoter 107 a 61 c 74 g 75 t

BASE COUNT 107 a 61 c 74 g 75 t

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Matches 60; Conservative 0; Mismatches 0;

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RESULT 3
AX036738
LOCUS AX036738 348 bp DNA linear PAT 16-NOV-2000
DEFINITION Sequence 4 from Patent WO0058485.
ACCESSION AX036738
VERSION AX036738.1 GI:11226247
KEYWORDS
SOURCE synthetic construct.
ORGANISM synthetic construct.
REFERENCE 1 (bases 1 to 348)
AUTHORS Rance, I., Theisen, M., and Gruber, V.
TITLE ChimERIC expression promoters originating from commelina yellow
mottle virus and cassava vein mosaic virus
Patent: WO 0058485-A 4 05-OCT-2000;
JOURNAL MERISTEM THERAPEUTICS (FR) ; RANCE IANN (FR) ; THEISEN MANFRED (FR)

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/note="promoter Mp1116"

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BASE COUNT 116 a 70 c 78 g 84 t

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LOCUS AX036755 392 bp DNA linear PAT 16-NOV-2000
DEFINITION Sequence 21 from Patent WO0058485.
ACCESSION AX036755
VERSION AX036755.1 GI:11226264
KEYWORDS
SOURCE synthetic construct.
ORGANISM synthetic construct.
REFERENCE 1 (bases 1 to 392)
AUTHORS Rance, I., Theisen, M., and Gruber, V.
TITLE ChimERIC expression promoters originating from commelina yellow
mottle virus and cassava vein mosaic virus
Patent: WO 0058485-A 21 05-OCT-2000;
JOURNAL MERISTEM THERAPEUTICS (FR) ; RANCE IANN (FR) ; THEISEN MANFRED (FR)

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Promoter 127 a 80 c 87 g 98 t

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RESULT 5
AX036753
LOCUS AX036753 393 bp DNA linear PAT 16-NOV-2000
DEFINITION Sequence 19 from Patent WO0058485.
ACCESSION AX036753
VERSION AX036753.1 GI:11226262
KEYWORDS
SOURCE synthetic construct.
ORGANISM synthetic construct.
REFERENCE 1 (bases 1 to 393)
AUTHORS Rance, I., Theisen, M., and Gruber, V.
TITLE ChimERIC expression promoters originating from commelina yellow
mottle virus and cassava vein mosaic virus
Patent: WO 0058485-A 19 05-OCT-2000;
JOURNAL MERISTEM THERAPEUTICS (FR) ; RANCE IANN (FR) ; THEISEN MANFRED (FR)

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/note="promoter Mp1116"

Promoter 1.393
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Best Local Similarity 100.0%; Pred. No. 3.4e-10;
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RESULT 6
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LOCUS Sequence 20 from Patent WO0058485.
ACCESSION AX036754
VERSION AX036754.1 GI:11226263
KEYWORDS
SOURCE synthetic construct.
ORGANISM artificial sequences.
REFERENCE 1 (bases 1 to 462)
AUTHORS Rance,I., Theisen,M. and Gruber,V.
TITLE ChimERIC expression promoters originating from commelina yellow mottle virus and cassava vein mosaic virus
JOURNAL Patent: WO 0058485-A 20 05-OCT-2000;
MERISTEM THERAPEUTICS (FR) ; RANCE IANN (FR) ; THEISEN MANFRED (FR) ; GRUBER VERONIQUE (FR)
LOCATION/Qualifiers

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/note="promoter MPRI163"

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Best Local Similarity 100.0%; Pred. No. 3.4e-10;
Matches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 7
AX036756 600 bp DNA linear PAT 16-NOV-2000
LOCUS Sequence 22 from Patent WO0058485.
ACCESSION AX036756
VERSION AX036756.1 GI:11226265
KEYWORDS
SOURCE synthetic construct.
ORGANISM artificial sequences.
REFERENCE 1 (bases 1 to 600)
AUTHORS Rance,I., Theisen,M. and Gruber,V.
TITLE ChimERIC expression promoters originating from commelina yellow mottle virus and cassava vein mosaic virus
JOURNAL Patent: WO 0058485-A 22 05-OCT-2000;
MERISTEM THERAPEUTICS (FR) ; RANCE IANN (FR) ; THEISEN MANFRED (FR) ; GRUBER VERONIQUE (FR)
LOCATION/Qualifiers

FEATURES
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/note="promoter MPRI165"

BASE COUNT 188 a 111 c 147 g 154 t
ORIGIN

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Matches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 8
AX093047 9285 bp DNA linear PAT 30-MAR-2001
LOCUS Sequence 52 from Patent WO0118192.
ACCESSION AX093047
VERSION AX093047.1 GI:13509522
KEYWORDS
SOURCE synthetic construct.
ORGANISM artificial sequences.
REFERENCE 1 (bases 1 to 9285)
AUTHORS Gruber,V. and Comeau,D.
TITLE Synthetic vectors, transgenic plants containing them, and methods for obtaining them
JOURNAL Patent: WO 0118192-A 52 15-MAR-2001;
MERISTEM THERAPEUTICS (FR)
LOCATION/Qualifiers

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/note="PMRT1336"

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RESULT 9
AX093052 15077 bp DNA linear PAT 30-MAR-2001
LOCUS Sequence 57 from Patent WO0118192.
ACCESSION AX093052
VERSION AX093052.1 GI:13509527
KEYWORDS
SOURCE synthetic construct.
ORGANISM artificial sequences.
REFERENCE 1 (bases 1 to 15077)
AUTHORS Gruber,V. and Comeau,D.
TITLE Synthetic vectors, transgenic plants containing them, and methods for obtaining them
JOURNAL Patent: WO 0118192-A 57 15-MAR-2001;
MERISTEM THERAPEUTICS (FR)
LOCATION/Qualifiers

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/note="PMRT1342"

misc_feature 1
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ORIGIN

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RESULT 10
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LOCUS Sequence 7 from Patent WO0058485.
DEFINITION
ACCESSION AX036741
VERSION AX036741.1 GI:11226250
KEYWORDS
SOURCE synthetic construct.
ORGANISM
ARTIFICIAL SEQUENCES
REFERENCE 1 (bases 1 to 301)
AUTHORS Rance, I., Theisen, M. and Gruber, V.
TITLE ChimERIC EXPRESSION PROMOTERS ORIGINATING FROM COMMELINA YELLOW
JOURNAL mottle virus and cassava vein mosaic virus
PATENT: WO 0058485-A 7 05-OCT-2000;
MERISTEM THERAPEUTICS (FR) ; RANCE IANN (FR) ; THEISEN MANFRED (FR)
; GRUBER VERONIQUE (FR)
LOCATION/Qualifiers

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AX036739 AX036739 371 bp DNA linear PAT 16-NOV-2000
LOCUS Sequence 5 from Patent WO0058485.
DEFINITION
ACCESSION AX036739
VERSION AX036739.1 GI:11226248
KEYWORDS
SOURCE synthetic construct.
ORGANISM
ARTIFICIAL SEQUENCES
REFERENCE 1 (bases 1 to 371)
AUTHORS Rance, I., Theisen, M. and Gruber, V.
TITLE ChimERIC EXPRESSION PROMOTERS ORIGINATING FROM COMMELINA YELLOW
JOURNAL mottle virus and cassava vein mosaic virus
PATENT: WO 0058485-A 5 05-OCT-2000;
MERISTEM THERAPEUTICS (FR) ; RANCE IANN (FR) ; THEISEN MANFRED (FR)
; GRUBER VERONIQUE (FR)
LOCATION/Qualifiers

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BASE COUNT 122 a 68 c 89 g 92 t
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Matches 56; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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RESULT 12
AX036740 AX036740 398 bp DNA linear PAT 16-NOV-2000
LOCUS Sequence 6 from Patent WO0058485.
DEFINITION
ACCESSION AX036740
VERSION AX036740.1 GI:11226249
KEYWORDS
SOURCE synthetic construct.
ORGANISM
ARTIFICIAL SEQUENCES
REFERENCE 1 (bases 1 to 398)
AUTHORS Rance, I., Theisen, M. and Gruber, V.
TITLE ChimERIC EXPRESSION PROMOTERS ORIGINATING FROM COMMELINA YELLOW
JOURNAL mottle virus and cassava vein mosaic virus
PATENT: WO 0058485-A 6 05-OCT-2000;
MERISTEM THERAPEUTICS (FR) ; RANCE IANN (FR) ; THEISEN MANFRED (FR)
; GRUBER VERONIQUE (FR)
LOCATION/Qualifiers

FEATURES
source 1..398
/organism="synthetic construct"
/db_xref="taxon:32630"
/note="promoter MPr1147"

BASE COUNT 128 a 80 c 93 g 97 t
ORIGIN
promoter

Query Match 92.3%; Score 55.4; DB 6; Length 398;
Best Local Similarity 98.2%; Pred. No. 1.3e-08;
Matches 56; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4 CATGACACTGTGCGAATATTGAAGACGTAGACATGACACAAATGAAAAAGAA 60
Db 160 CATGCCACTGTGCGAATATTGAAGACGTAGACATGACACAAATGAAAAAGAA 216

RESULT 13
AX036759 AX036759 472 bp DNA linear PAT 16-NOV-2000
LOCUS Sequence 25 from Patent WO0058485.
DEFINITION
ACCESSION AX036759
VERSION AX036759.1 GI:11226268
KEYWORDS
SOURCE synthetic construct.
ORGANISM
ARTIFICIAL SEQUENCES
REFERENCE 1 (bases 1 to 472)
AUTHORS Rance, I., Theisen, M. and Gruber, V.
TITLE ChimERIC EXPRESSION PROMOTERS ORIGINATING FROM COMMELINA YELLOW
JOURNAL mottle virus and cassava vein mosaic virus
PATENT: WO 0058485-A 25 05-OCT-2000;
MERISTEM THERAPEUTICS (FR) ; RANCE IANN (FR) ; THEISEN MANFRED (FR)
; GRUBER VERONIQUE (FR)
LOCATION/Qualifiers

FEATURES
source 1..472
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/db_xref="taxon:32630"
/note="promoter MPr1169"

BASE COUNT 149 a 92 c 112 g 119 t
ORIGIN
promoter

Query Match 92.3%; Score 55.4; DB 6; Length 472;
Best Local Similarity 98.2%; Pred. No. 1.3e-08;
Matches 56; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 CATGACACTCTGTGCGAATATTGAAGACGTAGACACTGACGACCAACATGAAAGAA 60
 Db 160 CATGCACTCTGTGCGAATATTGAAGACGTAGACACTGACGACCAACATGAAAGAA 216

RESULT 14

AX036758 541 bp DNA linear PAT 16-NOV-2000
 LOCUS Sequence 24 from Patent WO0058485.
 DEFINITION AX036758
 ACCESSION AX036758
 VERSION AX036758.1 GI:11226267
 KEYWORDS
 SOURCE synthetic construct.
 ORGANISM synthetic construct.

REFERENCE 1 (bases 1 to 541)
 AUTHORS Rance,I., Theisen,M. and Gruber,V.
 TITLE ChimERIC expression promoters originating from commelina yellow
 JOURNAL mottle virus and cassava vein mosaic virus
 Patent: WO 0058485-A 24 05-OCT-2000;
 MERISTEM THERAPEUTICS (FR) ; RANCE IANN (FR) ; THEISEN MANFRED (FR)
 ; GRUBER VERONIQUE (FR)

FEATURES

source
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 /organism="synthetic construct"
 /db_xref="taxon:32630"
 /note="promoter MPr1168"

Promoter 1..541
 BASE COUNT 169 a 104 c 130 g 138 t
 ORIGIN

Query Match 92.3%; Score 55.4; DB 6; Length 541;
 Best Local Similarity 98.2%; Pred. No. 1.3e-08;
 Matches 56; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 CATGACACTCTGTGCGAATATTGAAGACGTAGACACTGACGACCAACATGAAAGAA 60
 Db 160 CATGCACTCTGTGCGAATATTGAAGACGTAGACACTGACGACCAACATGAAAGAA 216

RESULT 15

AX036757 604 bp DNA linear PAT 16-NOV-2000
 LOCUS Sequence 23 from Patent WO0058485.
 DEFINITION AX036757
 ACCESSION AX036757
 VERSION AX036757.1 GI:11226266
 KEYWORDS
 SOURCE synthetic construct.
 ORGANISM synthetic construct.

REFERENCE 1 (bases 1 to 604)
 AUTHORS Rance,I., Theisen,M. and Gruber,V.
 TITLE ChimERIC expression promoters originating from commelina yellow
 JOURNAL mottle virus and cassava vein mosaic virus
 Patent: WO 0058485-A 23 05-OCT-2000;
 MERISTEM THERAPEUTICS (FR) ; RANCE IANN (FR) ; THEISEN MANFRED (FR)
 ; GRUBER VERONIQUE (FR)

FEATURES

source
 1..604
 /organism="synthetic construct"
 /db_xref="taxon:32630"
 /note="promoter MPr1167"

Promoter 1..604
 BASE COUNT 186 a 116 c 145 g 157 t
 ORIGIN

Query Match 92.3%; Score 55.4; DB 6; Length 604;
 Best Local Similarity 98.2%; Pred. No. 1.3e-08;
 Matches 56; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 CATGACACTCTGTGCGAATATTGAAGACGTAGACACTGACGACCAACATGAAAGAA 60
 Db 160 CATGCACTCTGTGCGAATATTGAAGACGTAGACACTGACGACCAACATGAAAGAA 216

Db 160 CATGCACTCTGTGCGAATATTGAAGACGTAGACACTGACGACCAACATGAAAGAA 216
 Search completed: May 24, 2003, 14:52:19
 Job time : 340.194 secs

GenCore version 5.1.4.p5 4578
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OM nucleic - nucleic search, using sw model

Run on: May 24, 2003, 07:18:51 ; Search time 103.548 Seconds
(without alignments)
1304.896 Million cell updates/sec

Title: US-09-963-803-9

Perfect score: 60

Sequence: 1 agccatgacactctgtcgcga.....gacacacacatgaagaaga 60

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 2185239 seqs, 112599159 residues 4370478

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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23: /SID52/gcgdata/geneSeq/geneSeq-emb1/NA2001B.DAT.*

24: /SID52/gcgdata/geneSeq/geneSeq-emb1/NA2002.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	60	100.0	60	21	AAA96843
2	60	100.0	317	21	AAA96837
3	60	100.0	348	21	AAA96838
4	60	100.0	392	21	AAA96855
5	60	100.0	393	21	AAA96853
6	60	100.0	462	21	AAA96854
7	60	100.0	600	21	AAA96856
8	55.4	92.3	301	21	AAA96841
9	55.4	92.3	371	21	AAA96839

10	55.4	92.3	398	21	AAA96840	Nucleotide sequenc
11	55.4	92.3	472	21	AAA96859	Nucleotide sequenc
12	55.4	92.3	541	21	AAA96858	Nucleotide sequenc
13	55.4	92.3	604	21	AAA96857	Nucleotide sequenc
14	40.4	67.3	392	19	AAV14019	CSVMV promoter CVP
15	40.4	67.3	408	19	AAV14031	CSVMV promoter pde
16	40.4	67.3	411	19	AAV14021	CSVMV promoter pB.
17	40.4	67.3	418	19	AAV14032	CSVMV promoter pde
18	40.4	67.3	441	19	AAV14033	CSVMV promoter pde
19	40.4	67.3	458	19	AAV14028	CSVMV promoter pde
20	40.4	67.3	468	19	AAV14029	CSVMV promoter pde
21	40.4	67.3	476	19	AAV14053	CSVMV promoter . C
22	40.4	67.3	491	19	AAV14030	CSVMV promoter pde
23	40.4	67.3	515	21	AAA96836	Promoter from inte
24	40.4	67.3	515	22	AAE5505	Nucleotide sequenc
25	40.4	67.3	524	19	AAV14020	CSVMV promoter CVP
26	40.4	67.3	526	19	AAV14018	CSVMV promoter pA.
27	40.4	67.3	532	22	AAV11575	Cassava Vein Mosai
28	40.4	67.3	593	22	AAE5507	Nucleotide sequenc
29	40.4	67.3	853	22	AAE5506	Nucleotide sequenc
30	40.4	67.3	857	22	AAE5508	Nucleotide sequenc
31	40.4	67.3	931	22	AAE5509	Nucleotide sequenc
32	40.4	67.3	931	22	AAE5510	Nucleotide sequenc
33	40.4	67.3	931	22	AAE5510	Nucleotide sequenc
34	40.4	67.3	1839	24	ABL57988	4-Hydroxyphenylpyr
35	40.4	67.3	4677	24	ABL57989	4-Hydroxyphenylpyr
36	40.4	67.3	8187	24	ABL58082	4-Hydroxyphenylpyr
37	40.4	67.3	8340	24	ABA04755	Binary vector PAGI
38	40.4	67.3	8340	24	ABD24139	PAGI002 binary ve
39	40.4	67.3	12241	24	ABQ73049	Tomato anthocyanin
40	40.4	67.3	12241	24	AA036732	Binary vector DNA
41	37.2	62.0	305	19	AAV14022	CSVMV promoter pC.
42	37.2	62.0	420	19	AAV14026	CSVMV promoter pde
43	25.2	42.0	2022	21	AAE46193	Arabidopsis thalia
44	25.2	42.0	2525	21	AAE45306	Arabidopsis thalia
45	25.2	42.0	2547	21	AAE40898	Arabidopsis thalia

ALIGNMENTS

RESULT 1	AAA96843	standard; DNA; 60 BP.
ID	AAA96843	
AC	AAA96843	
XX	19-FEB-2001	(first entry)
DT		
DE		Directional desoxynucleotide building block 52.
XX		
KW	Promoter; intergenic region; Commelina yellow mottle virus;	
KW	chimeric expression promoter; plant vascular expression promoter;	
KW	plant green tissue expression promoter; Cassava vein mosaic virus;	
KW	transgenic plant; ss.	
XX		
OS	Synthetic.	
XX		
FN	W0200058485-A1.	
PD	05-OCT-2000.	
XX		
PF	29-MAR-2000; 2000WO-IB00370.	
XX		
FR	29-MAR-1999; 99FR-0003925.	
XX		
PA	(MERI-) MERISTEM THERAPEUTICS.	
XX		
PI	Rance I, Gruber V, Theisen M;	
XX		
DR	WPI: 2000-647238/62.	
XX		
PT	Chimeric expression promoter for transgenic plant production, comprises	

PT sequence from promoter comprising vascular expression region replaced
PT with sequence from promoter comprising green tissue expression region
XX
XX
PS Disclosure; Page 23; 91pp; English.
XX
CC The present sequence represents a directional desoxynucleotide building
CC block, which was used to construct chimeric promoters of the invention.
CC The specification describes chimeric expression promoters. These
CC chimeric promoters comprise a nucleic acid sequence which is derived
CC from a first plant promoter, in which a plant vascular expression
CC promoter region is replaced with a nucleic acid sequence derived from
CC a second plant promoter comprising a plant green tissue expression
CC promoter region. Preferably, the first plant promoter originates from
CC Comellina yellow mottle virus, and the second plant promoter originates
CC from the Cassava vein mosaic virus. Especially, the promoters are
CC derived from intergenic regions. The chimeric promoters are useful
CC for producing transgenic plants.
XX
SQ Sequence 60 BP; 25 A; 12 C; 13 G; 10 T; 0 other;
Query Match 100.0%; Score 60; DB 21; Length 60;
Best Local Similarity 100.0%; Pred. No. 3.2e-12;
Matches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 AGCCATGACACTCTGTGCGAATATTGAAGACGTAAAGCAGACAGCAACAATGAAAAAGAA 60
DB 1 AGCCATGACACTCTGTGCGAATATTGAAGACGTAAAGCAGACAGCAACAATGAAAAAGAA 60
RESULT 2
AAA96837
ID AAA96837 standard; DNA: 317 BP.
XX
XX AAA96837;
XX
DT 19-FEB-2001 (first entry)
XX
DE Nucleotide sequence of chimeric expression promoter MP11116.
XX
XX Promoter; intergenic region; Comellina yellow mottle virus;
KM chimeric expression promoter; plant vascular expression promoter;
KM plant green tissue expression promoter; Cassava vein mosaic virus;
KM transgenic plant; chimera; ss.
XX
XX Chimeric - Comellina yellow mottle virus.
OS Chimeric - Cassava vein mosaic virus.
XX
XX WO200058485-A1.
XX
PD 05-OCT-2000.
XX
XX 29-MAR-2000; 2000MO-IB00370.
XX
XX 29-MAR-1999; 99FR-0003925.
XX
XX (MERI-) MERISTEM THERAPEUTICS.
XX
XX Rance I, Gruber V, Theisen M;
XX
XX WPI; 2000-647238/62.
XX
XX Chimeric expression promoter for transgenic plant production, comprises
PT sequence from promoter comprising vascular expression region replaced
PT with sequence from promoter comprising green tissue expression region
XX
XX
PS Claim 5; Page 81; 91pp; English.
XX
XX The present sequence represents a chimeric promoter of the invention.
CC The specification describes chimeric expression promoters. These
CC chimeric promoters comprise a nucleic acid sequence which is derived
CC from a first plant promoter, in which a plant vascular expression
CC promoter region is replaced with a nucleic acid sequence derived from
CC a second plant promoter comprising a plant green tissue expression
CC promoter region. Preferably, the first plant promoter originates from
CC Comellina yellow mottle virus, and the second plant promoter originates
CC from the Cassava vein mosaic virus. Especially, the promoters are
CC derived from intergenic regions. The chimeric promoters are useful
CC for producing transgenic plants.
XX
SQ Sequence 60 BP; 25 A; 12 C; 13 G; 10 T; 0 other;

CC promoter region is replaced with a nucleic acid sequence derived from
CC a second plant promoter comprising a plant green tissue expression
CC promoter region. Preferably, the first plant promoter originates from
CC Comellina yellow mottle virus, and the second plant promoter originates
CC from the Cassava vein mosaic virus. Especially, the promoters are
CC derived from intergenic regions. The chimeric promoters are useful
CC for producing transgenic plants.
XX
SQ Sequence 317 BP; 107 A; 61 C; 74 G; 75 T; 0 other;
Query Match 100.0%; Score 60; DB 21; Length 317;
Best Local Similarity 100.0%; Pred. No. 4.6e-12;
Matches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 AGCCATGACACTCTGTGCGAATATTGAAGACGTAAAGCAGACAGCAACAATGAAAAAGAA 60
DB 73 AGCCATGACACTCTGTGCGAATATTGAAGACGTAAAGCAGACAGCAACAATGAAAAAGAA 132
RESULT 3
AAA96838
ID AAA96838 standard; DNA: 348 BP.
XX
XX AAA96838;
XX
DT 19-FEB-2001 (first entry)
XX
DE Nucleotide sequence of chimeric expression promoter MP11117.
XX
XX Promoter; intergenic region; Comellina yellow mottle virus;
KM chimeric expression promoter; plant vascular expression promoter;
KM plant green tissue expression promoter; Cassava vein mosaic virus;
KM transgenic plant; chimera; ss.
XX
XX Chimeric - Comellina yellow mottle virus.
OS Chimeric - Cassava vein mosaic virus.
XX
XX WO200058485-A1.
XX
PD 05-OCT-2000.
XX
XX 29-MAR-2000; 2000MO-IB00370.
XX
XX 29-MAR-1999; 99FR-0003925.
XX
XX (MERI-) MERISTEM THERAPEUTICS.
XX
XX Rance I, Gruber V, Theisen M;
XX
XX WPI; 2000-647238/62.
XX
XX Chimeric expression promoter for transgenic plant production, comprises
PT sequence from promoter comprising vascular expression region replaced
PT with sequence from promoter comprising green tissue expression region
XX
XX
PS Claim 5; Page 81; 91pp; English.
XX
XX The present sequence represents a chimeric promoter of the invention.
CC The specification describes chimeric expression promoters. These
CC chimeric promoters comprise a nucleic acid sequence which is derived
CC from a first plant promoter, in which a plant vascular expression
CC promoter region is replaced with a nucleic acid sequence derived from
CC a second plant promoter comprising a plant green tissue expression
CC promoter region. Preferably, the first plant promoter originates from
CC Comellina yellow mottle virus, and the second plant promoter originates
CC from the Cassava vein mosaic virus. Especially, the promoters are
CC derived from intergenic regions. The chimeric promoters are useful
CC for producing transgenic plants.
XX
SQ Sequence 348 BP; 116 A; 70 C; 78 G; 84 T; 0 other;
Query Match 100.0%; Score 60; DB 21; Length 348;

Best Local Similarity 100.0%; Pred. No. 4.7e-12;
Matches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGCCATGACACTCTGTGGGAATATTGAAGACGTAGCACTGACGCAACAATGAAAAAGA 60
DB 107 AGCCATGACACTCTGTGGGAATATTGAAGACGTAGCACTGACGCAACAATGAAAAAGA 166

RESULT 4
ID AAA96855 standard; DNA; 392 BP.

AC AAA96855;

DT 19-FEB-2001 (first entry)

DE Nucleotide sequence of chimeric expression promoter MPr1164.

XX Promoter; intergenic region; Commelina yellow mottle virus;

KW chimeric expression promoter; plant vascular expression promoter;

KM plant green tissue expression promoter; Cassava vein mosaic virus;

XX transgenic plant; chimera; ss.

OS Chimeric - Commelina yellow mottle virus.

XX Chimeric - Cassava vein mosaic virus.

PN WO200058485-A1.

XX 05-OCT-2000.

PF 29-MAR-2000; 2000WO-IB00370.

XX 29-MAR-1999; 99FR-0003925.

XX (MERI-) MERISTEM THERAPEUTICS.

PI Rance I, Gruber V, Theisen M;

XX WPI; 2000-647238/62.

XX Claim 5; Page 86; 91pp; English.

CC The present sequence represents a chimeric promoter of the invention.

CC The specification describes chimeric expression promoters. These

CC chimeric promoters comprise a nucleic acid sequence which is derived

CC from a first plant promoter, in which a plant vascular expression

CC promoter region is replaced with a nucleic acid sequence derived from

CC a second plant promoter comprising a plant green tissue expression

CC promoter region. Preferably, the first plant promoter originates from

CC Commelina yellow mottle virus, and the second plant promoter originates

CC from the Cassava vein mosaic virus. Especially, the promoters are

CC derived from intergenic regions. The chimeric promoters are useful

CC for producing transgenic plants.

XX SQ Sequence 392 BP; 127 A; 80 C; 87 G; 98 T; 0 other;

Query Match 100.0%; Score 60; DB 21; Length 392;
Best Local Similarity 100.0%; Pred. No. 4.8e-12;
Matches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX AAA96853;

DT 19-FEB-2001 (first entry)

DE Nucleotide sequence of chimeric expression promoter MPr1162.

XX Promoter; intergenic region; Commelina yellow mottle virus;

KW chimeric expression promoter; plant vascular expression promoter;

KM plant green tissue expression promoter; Cassava vein mosaic virus;

XX transgenic plant; chimera; ss.

OS Chimeric - Commelina yellow mottle virus.

XX Chimeric - Cassava vein mosaic virus.

PN WO200058485-A1.

XX 05-OCT-2000.

PF 29-MAR-2000; 2000WO-IB00370.

XX 29-MAR-1999; 99FR-0003925.

XX (MERI-) MERISTEM THERAPEUTICS.

PI Rance I, Gruber V, Theisen M;

XX WPI; 2000-647238/62.

XX Claim 5; Page 85; 91pp; English.

CC The present sequence represents a chimeric promoter of the invention.

CC The specification describes chimeric expression promoters. These

CC chimeric promoters comprise a nucleic acid sequence which is derived

CC from a first plant promoter, in which a plant vascular expression

CC promoter region is replaced with a nucleic acid sequence derived from

CC a second plant promoter comprising a plant green tissue expression

CC promoter region. Preferably, the first plant promoter originates from

CC Commelina yellow mottle virus, and the second plant promoter originates

CC from the Cassava vein mosaic virus. Especially, the promoters are

CC derived from intergenic regions. The chimeric promoters are useful

CC for producing transgenic plants.

XX SQ Sequence 393 BP; 128 A; 75 C; 93 G; 97 T; 0 other;

Query Match 100.0%; Score 60; DB 21; Length 393;
Best Local Similarity 100.0%; Pred. No. 4.8e-12;
Matches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGCCATGACACTCTGTGGGAATATTGAAGACGTAGCACTGACGCAACAATGAAAAAGA 60
DB 75 AGCCATGACACTCTGTGGGAATATTGAAGACGTAGCACTGACGCAACAATGAAAAAGA 134

RESULT 6
ID AAA96854 standard; DNA; 462 BP.

AC AAA96854;

DT 19-FEB-2001 (first entry)

DE Nucleotide sequence of chimeric expression promoter MPr1163.

XX Promoter; intergenic region; Commelina yellow mottle virus;

KW chimeric expression promoter; plant vascular expression promoter;

KM plant green tissue expression promoter; Cassava vein mosaic virus;

XX transgenic plant; chimera; ss.

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XX OS Chimeric - Commelina yellow mottle virus.
XX OS Chimeric - Cassava vein mosaic virus.
XX PN WO200058485-A1.
XX PD 05-OCT-2000.
XX PF 29-MAR-2000; 2000MO-IB00370.
XX PR 29-MAR-1999; 99FR-0003925.
XX
XX PA (MERI-) MERISTEM THERAPEUTICS.
XX PI Rance I, Gruber V, Theisen M;
XX DR WPI; 2000-647238/62.
XX
XX PT Chimeric expression promoter for transgenic plant production, comprises
XX PT sequence from promoter comprising vascular expression region replaced
XX PT with sequence from promoter comprising green tissue expression region
XX
XX PS Claim 5; Page 86; 91pp; English.
XX
XX CC The present sequence represents a chimeric promoter of the invention.
XX CC The specification describes chimeric expression promoters. These
XX CC chimeric promoters comprise a nucleic acid sequence which is derived
XX CC from a first plant promoter, in which a plant vascular expression
XX CC promoter region is replaced with a nucleic acid sequence derived from
XX CC a second plant promoter comprising a plant green tissue expression
XX CC promoter region. Preferably, the first plant promoter originates from
XX CC Commelina yellow mottle virus, and the second plant promoter originates
XX CC from the Cassava vein mosaic virus. Especially, the promoters are
XX CC derived from intergenic regions. The chimeric promoters are useful
XX CC for producing transgenic plants.
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XX SQ Sequence 462 BP; 148 A; 87 C; 111 G; 116 T; 0 other;
XX
XX Query Match 100.0%; Score 60; DB 21; Length 462;
XX Best Local Similarity 100.0%; Pred. No. 5e-12;
XX Matches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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XX QY 1 AGCCATGACACTCTGTCGCAATATTGAAGACGTAGACAGCAGCAACAATGAAAAAGAA 60
XX |
XX DB 75 AGCCATGACACTCTGTCGCAATATTGAAGACGTAGACAGCAGCAACAATGAAAAAGAA 134
XX
XX RESULT 7
XX ID AAA96856 standard; DNA; 600 BP.
XX
XX AC AAA96856;
XX
XX DT 19-FEB-2001 (first entry)
XX
XX DE Nucleotide sequence of chimeric expression promoter MP11165.
XX
XX KW Promoter; intergenic region; Commelina yellow mottle virus;
XX KW chimeric expression promoter; plant vascular expression promoter;
XX KW plant green tissue expression promoter; Cassava vein mosaic virus;
XX KW transgenic plant; chimera; ss.
XX
XX OS Chimeric - Commelina yellow mottle virus.
XX OS Chimeric - Cassava vein mosaic virus.
XX PN WO200058485-A1.
XX
XX PD 05-OCT-2000.
XX
XX PF 29-MAR-2000; 2000MO-IB00370.
XX
XX PR 29-MAR-1999; 99FR-0003925.
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XX PA (MERI-) MERISTEM THERAPEUTICS.
XX PI Rance I, Gruber V, Theisen M;
XX DR WPI; 2000-647238/62.
XX
XX PT Chimeric expression promoter for transgenic plant production, comprises
XX PT sequence from promoter comprising vascular expression region replaced
XX PT with sequence from promoter comprising green tissue expression region
XX
XX PS Claim 5; Page 86-87; 91pp; English.
XX
XX CC The present sequence represents a chimeric promoter of the invention.
XX CC The specification describes chimeric expression promoters. These
XX CC chimeric promoters comprise a nucleic acid sequence which is derived
XX CC from a first plant promoter, in which a plant vascular expression
XX CC promoter region is replaced with a nucleic acid sequence derived from
XX CC a second plant promoter comprising a plant green tissue expression
XX CC promoter region. Preferably, the first plant promoter originates from
XX CC Commelina yellow mottle virus, and the second plant promoter originates
XX CC from the Cassava vein mosaic virus. Especially, the promoters are
XX CC derived from intergenic regions. The chimeric promoters are useful
XX CC for producing transgenic plants.
XX
XX SQ Sequence 600 BP; 188 A; 111 C; 147 G; 154 T; 0 other;
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XX Query Match 100.0%; Score 60; DB 21; Length 600;
XX Best Local Similarity 100.0%; Pred. No. 5.3e-12;
XX Matches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 AGCCATGACACTCTGTCGCAATATTGAAGACGTAGACAGCAGCAACAATGAAAAAGAA 60
XX |
XX DB 75 AGCCATGACACTCTGTCGCAATATTGAAGACGTAGACAGCAGCAACAATGAAAAAGAA 134
XX
XX RESULT 8
XX ID AAA96841 standard; DNA; 301 BP.
XX
XX AC AAA96841;
XX
XX DT 19-FEB-2001 (first entry)
XX
XX DE Nucleotide sequence of chimeric expression promoter MP11154.
XX
XX KW Promoter; intergenic region; Commelina yellow mottle virus;
XX KW chimeric expression promoter; plant vascular expression promoter;
XX KW plant green tissue expression promoter; Cassava vein mosaic virus;
XX KW transgenic plant; chimera; ss.
XX
XX OS Chimeric - Commelina yellow mottle virus.
XX OS Chimeric - Cassava vein mosaic virus.
XX PN WO200058485-A1.
XX
XX PD 05-OCT-2000.
XX
XX PF 29-MAR-2000; 2000MO-IB00370.
XX
XX PR 29-MAR-1999; 99FR-0003925.
XX
XX PA (MERI-) MERISTEM THERAPEUTICS.
XX PI Rance I, Gruber V, Theisen M;
XX DR WPI; 2000-647238/62.
XX
XX PT Chimeric expression promoter for transgenic plant production, comprises
XX PT sequence from promoter comprising vascular expression region replaced
XX PT with sequence from promoter comprising green tissue expression region
```


XX Claim 5; Page 82; 91pp; English.
PS
XX
CC The present sequence represents a chimeric promoter of the invention.
CC The specification describes chimeric expression promoters. These
CC chimeric promoters comprise a nucleic acid sequence which is derived
CC from a first plant promoter, in which a plant vascular expression
CC promoter region is replaced with a nucleic acid sequence derived from
CC a second plant promoter comprising a plant green tissue expression
CC promoter region. Preferably, the first plant promoter originates from
CC Commelina yellow mottle virus, and the second plant promoter originates
CC from the Cassava vein mosaic virus. Especially, the promoters are
CC derived from intergenic regions. The chimeric promoters are useful
CC for producing transgenic plants.
XX
SQ Sequence 301 BP; 98 A; 54 C; 74 G; 75 T; 0 other;
Query Match 92.3%; Score 55.4; DB 21; Length 301;
Best Local Similarity 98.2%; Pred. No. 2e-10;
Matches 56; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
OY 4 CATGACACTCTGTGCGAATATTGAAGACGTAGCAGTGCAGCAACAATGAAAGAA 60
DB 63 CATGCCACTCTGTGCGAATATTGAAGACGTAGCAGTGCAGCAACAATGAAAGAA 119
RESULT 9
AAA96839
ID AAA96839 standard; DNA; 371 BP.
XX
AC AAA96839;
XX
DT 19-FEB-2001 (first entry)
XX
DE Nucleotide sequence of chimeric expression promoter MP1146.
XX
KM Promoter; intergenic region; Commelina yellow mottle virus;
KM chimeric expression promoter; plant vascular expression promoter;
KW plant green tissue expression promoter; Cassava vein mosaic virus;
KW transgenic plant; chimera; ss.
XX
OS Chimeric - Commelina yellow mottle virus.
OS Chimeric - Cassava vein mosaic virus.
XX
PN MO200058485-A1.
XX
PD 05-OCT-2000.
XX
PF 29-MAR-2000; 2000MO-IB00370.
XX
PT 29-MAR-1999; 99FR-0003925.
XX
PR (MERIT-) MERISTEM THERAPEUTICS.
XX
PA Rance I, Gruber V, Theisen M;
XX
PI WPI; 2000-647238/62.
XX
DR WPI; 2000-647238/62.
XX
PT Chimeric expression promoter for transgenic plant production, comprises
PT sequence from promoter comprising vascular expression region replaced
PT with sequence from promoter comprising green tissue expression region
XX
PS Claim 5; Page 81; 91pp; English.
XX
CC The present sequence represents a chimeric promoter of the invention.
CC The specification describes chimeric expression promoters. These
CC chimeric promoters comprise a nucleic acid sequence which is derived
CC from a first plant promoter, in which a plant vascular expression
CC promoter region is replaced with a nucleic acid sequence derived from
CC a second plant promoter comprising a plant green tissue expression
CC promoter region. Preferably, the first plant promoter originates from
CC Commelina yellow mottle virus, and the second plant promoter originates
CC from the Cassava vein mosaic virus, and the second plant promoter originates

CC from the Cassava vein mosaic virus. Especially, the promoters are
CC derived from intergenic regions. The chimeric promoters are useful
CC for producing transgenic plants.
XX
SQ Sequence 371 BP; 122 A; 68 C; 89 G; 92 T; 0 other;
Query Match 92.3%; Score 55.4; DB 21; Length 371;
Best Local Similarity 98.2%; Pred. No. 2.1e-10;
Matches 56; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
OY 4 CATGACACTCTGTGCGAATATTGAAGACGTAGCAGTGCAGCAACAATGAAAGAA 60
DB 130 CATGCCACTCTGTGCGAATATTGAAGACGTAGCAGTGCAGCAACAATGAAAGAA 186
RESULT 10
AAA96840
ID AAA96840 standard; DNA; 398 BP.
XX
AC AAA96840;
XX
DT 19-FEB-2001 (first entry)
XX
DE Nucleotide sequence of chimeric expression promoter MP1147.
XX
KM Promoter; intergenic region; Commelina yellow mottle virus;
KM chimeric expression promoter; plant vascular expression promoter;
KW plant green tissue expression promoter; Cassava vein mosaic virus;
KW transgenic plant; chimera; ss.
XX
OS Chimeric - Commelina yellow mottle virus.
OS Chimeric - Cassava vein mosaic virus.
XX
PN MO200058485-A1.
XX
PD 05-OCT-2000.
XX
PF 29-MAR-2000; 2000MO-IB00370.
XX
PT 29-MAR-1999; 99FR-0003925.
XX
PR (MERIT-) MERISTEM THERAPEUTICS.
XX
PA Rance I, Gruber V, Theisen M;
XX
PI WPI; 2000-647238/62.
XX
DR WPI; 2000-647238/62.
XX
PT Chimeric expression promoter for transgenic plant production, comprises
PT sequence from promoter comprising vascular expression region replaced
PT with sequence from promoter comprising green tissue expression region
XX
PS Claim 5; Page 82; 91pp; English.
XX
CC The present sequence represents a chimeric promoter of the invention.
CC The specification describes chimeric expression promoters. These
CC chimeric promoters comprise a nucleic acid sequence which is derived
CC from a first plant promoter, in which a plant vascular expression
CC promoter region is replaced with a nucleic acid sequence derived from
CC a second plant promoter comprising a plant green tissue expression
CC promoter region. Preferably, the first plant promoter originates from
CC Commelina yellow mottle virus, and the second plant promoter originates
CC from the Cassava vein mosaic virus. Especially, the promoters are
CC derived from intergenic regions. The chimeric promoters are useful
CC for producing transgenic plants.
XX
SQ Sequence 398 BP; 128 A; 80 C; 93 G; 97 T; 0 other;
Query Match 92.3%; Score 55.4; DB 21; Length 398;
Best Local Similarity 98.2%; Pred. No. 2.2e-10;
Matches 56; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
OY 4 CATGACACTCTGTGCGAATATTGAAGACGTAGCAGTGCAGCAACAATGAAAGAA 60

[illegible]

```

XX Nucleotide sequence of chimeric expression promoter MPr1168.
DE
XX Promoter; intergenic region; Commelina yellow mottle virus;
KW
XX Chimeric expression promoter; plant vascular expression promoter;
KW
XX plant green tissue expression promoter; Cassava vein mosaic virus;
XX transgenic plant; chimera; ss.
XX
OS Chimeric - Commelina yellow mottle virus.
OS
XX Chimeric - Cassava vein mosaic virus.
XX
XX WO20058485-A1.
XX
XX 05-OCT-2000.
XX
XX 29-MAR-2000; 2000WO-IB00370.
XX
XX 29-MAR-1999; 99FR-0003925.
XX
XX (MERT-) MERISTEM THERAPEUTICS.
XX
XX Rance I, Gruber V, Thelsen M;
XX
XX WPI; 2000-647238/62.
XX
XX Chimeric expression promoter for transgenic plant production, comprises
PT
XX sequence from promoter comprising vascular expression region replaced
PT
XX with sequence from promoter comprising green tissue expression region
PT
XX
XX Claim 5; Page 87-88; 91pp; English.
XX
XX The present sequence represents a chimeric promoter of the invention.
XX
XX The specification describes chimeric expression promoters. These
XX
XX chimeric promoters comprise a nucleic acid sequence which is derived
XX
XX from a first plant promoter, in which a plant vascular expression
XX
XX promoter region is replaced with a nucleic acid sequence derived from
XX
XX a second plant promoter comprising a plant green tissue expression
XX
XX promoter region. Preferably, the first plant promoter originates from
XX
XX Commelina yellow mottle virus, and the second plant promoter originates
XX
XX from the Cassava vein mosaic virus. Especially, the promoters are
XX
XX derived from intergenic regions. The chimeric promoters are useful
XX
XX for producing transgenic plants.
XX
XX Sequence 541 BP; 169 A; 104 C; 130 G; 138 T; 0 other:
XX
XX Query Match 92.3%; Score 55.4; DB 21; Length 541;
XX
XX Best Local Similarity 98.2%; Pred. No. 2.3e-10;
XX
XX Matches 56; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
XX 4 CATGCACTCTGTGGCAATATGGAAGCGTAGACACTGACGACAAATGAAAGAA 60
XX
XX ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
XX
XX Db 160 CATGCCACTCTGTGGCAATATGGAAGACGTAGACACTGACGACAAATGAAAGAA 216
XX
XX
XX RESULT 13
XX
XX ID AAA96857 standard; DNA; 604 BP.
XX
XX AAA96857;
XX
XX AC
XX
XX 19-FEB-2001 (first entry)
XX
XX DE Nucleotide sequence of chimeric expression promoter MPr1167.
XX
XX Promoter; intergenic region; Commelina yellow mottle virus;
KW
XX Chimeric expression promoter; plant vascular expression promoter;
KW
XX plant green tissue expression promoter; Cassava vein mosaic virus;
XX transgenic plant; chimera; ss.
XX
XX Chimeric - Commelina yellow mottle virus.
OS
XX Chimeric - Cassava vein mosaic virus.
XX

```

PN WO200058485-A1.
XX
PD 05-OCT-2000.
XX
PE 29-MAR-2000; 2000WO-IB00370.
XX
PR 29-MAR-1999; 99FR-0003925.
XX
PA (MERI-) MERISTEM THERAPEUTICS.
XX
PI Rance I, Gruber V, Theisen M;
XX WPI; 2000-647238/62.
DR
PT Chimeric expression promoter for transgenic plant production, comprises
PT sequence from promoter comprising vascular expression region replaced
PT with sequence from promoter comprising green tissue expression region
PT
PS
XX
PS Claim 5; Page 87; 91pp; English.
XX
CC The present sequence represents a chimeric promoter of the invention.
CC The specification describes chimeric expression promoters. These
CC chimeric promoters comprise a nucleic acid sequence which is derived
CC from a first plant promoter, in which a plant vascular expression
CC promoter region is replaced with a nucleic acid sequence derived from
CC a second plant promoter comprising a plant green tissue expression
CC promoter region. Preferably, the first plant promoter originates from
CC Commelina yellow mottle virus, and the second plant promoter originates
CC from the Cassava vein mosaic virus. Especially, the promoters are
CC derived from intergenic regions. The chimeric promoters are useful
CC for producing transgenic plants.
XX
SQ Sequence 604 BP; 186 A; 116 C; 145 G; 157 T; 0 other;
XX
Query Match 92.3%; Score 55.4; DB 21; Length 604;
Best Local Similarity 98.2%; Pred. No. 2.4e-10;
Matches 56; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
OY 4 CATGACACCTGTGCGAATATTGAGACGTAGACGTGACGACCAATGAAAAGAA 60
DB 160 CATGCCACTCTGTGCGAATATTGAGACGTAGACGTGACGACCAATGAAAAGAA 216
RESULT 14
AAV14019
ID AAV14019 standard; DNA; 392 BP.
XX
AC AAV14019;
XX
DT 18-JUN-1998 (first entry)
XX
DE CSVV promoter CVPL.
XX
KM Cassava vein mosaic virus; CSVV; promoter; cultivated crop;
KM tissue-specific expression control; transgenic plant; ss.
XX
OS Cassava vein mosaic virus.
XX
PN WO9748819-A1.
PD 24-DEC-1997.
XX
PF 20-JUN-1997; 97WO-US10376.
XX
PR 20-JUN-1996; 96US-0020129.
XX
PA (SCRI) SCRIPPS RES INST.
XX
PI Beachy RN, De Kochko A, Fauquet C, Verdaguer B;
XX WPI; 1998-063157/06.
XX

PT Cassava vein mosaic virus promoter - used to express heterologous
PT DNA sequences for producing transgenic plants having altered
PT phenotype(s)
XX
PS Claim 2; Page 74; 115pp; English.
XX
CC This sequence represents a cassava vein mosaic virus promoter, and
CC is a nucleic acid molecule of the invention. The promoter is capable of
CC initiating transcription of an operably linked heterologous nucleic acid
CC sequence in a plant cell. The CSVV promoters are active in both monocot
CC and dicot plant species, and therefore can be readily applied to a
CC variety of cultivated crops. Although generally constitutive, the
CC derivative promoters include promoters that can regulate expression in a
CC tissue-specific manner, and therefore are useful for controlling
CC expression of heterologous genes in a tissue-specific manner. The
CC promoters can be used for producing transgenic plants with an altered
XX phenotype.
XX
SQ Sequence 392 BP; 154 A; 64 C; 83 G; 91 T; 0 other;
XX
Query Match 67.3%; Score 40.4; DB 19; Length 392;
Best Local Similarity 97.6%; Pred. No. 5.1e-05;
Matches 41; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
OY 19 GAAATATTGAAGACGTAGACGTGACGACCAATGAAAAGAA 60
DB 143 GAATCTTGAAGACGTAGACGTGACGACCAATGAAAAGAA 184
RESULT 15
AAV14031
ID AAV14031 standard; DNA; 408 BP.
XX
AC AAV14031;
XX
DT 18-JUN-1998 (first entry)
XX
DE CSVV promoter pdeltaDE2.
XX
KM Cassava vein mosaic virus; CSVV; promoter; cultivated crop;
KM tissue-specific expression control; transgenic plant; ss.
XX
OS Cassava vein mosaic virus.
XX
PN WO9748819-A1.
PD 24-DEC-1997.
XX
PF 20-JUN-1997; 97WO-US10376.
XX
PR 20-JUN-1996; 96US-0020129.
XX
PA (SCRI) SCRIPPS RES INST.
XX
PI Beachy RN, De Kochko A, Fauquet C, Verdaguer B;
XX WPI; 1998-063157/06.
XX
PT Cassava vein mosaic virus promoter - used to express heterologous
PT DNA sequences for producing transgenic plants having altered
PT phenotype(s)
XX
PS Claim 2; Page 84-85; 115pp; English.
XX
CC This sequence represents a cassava vein mosaic virus promoter, and
CC is a nucleic acid molecule of the invention. The promoter is capable of
CC initiating transcription of an operably linked heterologous nucleic acid
CC sequence in a plant cell. The CSVV promoters are active in both monocot
CC and dicot plant species, and therefore can be readily applied to a
CC variety of cultivated crops. Although generally constitutive, the
CC derivative promoters include promoters that can regulate expression in a
CC tissue-specific manner, and therefore are useful for controlling
CC expression of heterologous genes in a tissue-specific manner. The

CC Promoters can be used for producing transgenic plants with an altered
phenotype.

XX
SQ Sequence 408 BP; 161 A; 61 C; 86 G; 100 T; 0 other;

Query Match 67.3%; Score 40.4; DB 19; Length 408;

Best Local Similarity 97.6%; Pred. No. 5.1e-05;
Matches 41; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 19 GAATATGTGAGACGCTAAGCACTGACGACAAACATGAAAGCA 60
|||||
Db 222 GAATCTGTGAGACGCTAAGCACTGACGACAAACATGAAAGCA 263

Search completed: May 24, 2003, 14:34:41
Job time : 104.548 secs

2120 ATATTGAGGGA

RESULT 2
US-09-085-199B-44/C
; Sequence 44, Application US/09085199B
; Patent No. 6235879
; GENERAL INFORMATION:
; APPLICANT: Hayden, Michael R.
; APPLICANT: Hackam, Abigail
; APPLICANT: Hug, A.H.M. Mahbubul
; APPLICANT: Chopra, Vikramjit Singh
; APPLICANT: Kalichman, Michael
; TITLE OF INVENTION: Apoptosis Modulators That Interact with the
; TITLE OF INVENTION: Huntington's Disease Gene
; NUMBER OF SEQUENCES: 44
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Opedahl & Larson
; STREET: PO Box 5270
; CITY: Ftisco
; STATE: CO
; COUNTRY: USA
; ZIP: 80443-5270
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.44 Kb storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: MS DOS 5.0
; SOFTWARE: Wordperfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/085,199B
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Larson, Marina T.
; REGISTRATION NUMBER: 32038
; REFERENCE/DOCKET NUMBER: UBC.P-0130S2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (970) 668-2050
; TELEFAX: (970) 668-2052
; INFORMATION FOR SEQ ID NO: 44:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3715
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: genomic DNA
; HYPOTHETICAL: no
; ANTI-SENSE: no
; ORIGINAL SOURCE:
; ORGANISM: human
; FEATURE:
; OTHER INFORMATION: exon 29 and partial cds of HIP1
; US-09-085-199B-44
Query Match 39.7%; Score 23.8; DB 4; Length 3715;
Best Local Similarity 66.7%; Pred. No. 7.3; Mismatches 17; Indels 0; Gaps 0;
Matches 34; Conservative 0; Mismatches 17; Indels 0; Gaps 0;
QY 10 ACTCTGCGCAATATTTGAAGACGTAAGACGACGACACACATGAAAGAA 60
DB 546 AGTTGTGCAATGATGAAACTGAAAGACTGAGAGAAAGAAAGAAAGAA 496
RESULT 3
US-09-085-199B-3/C
; Sequence 3, Application US/09085199B
; Patent No. 6235879
; GENERAL INFORMATION:
; APPLICANT: Hayden, Michael R.
; APPLICANT: Hackam, Abigail
; APPLICANT: Hug, A.H.M. Mahbubul
; APPLICANT: Chopra, Vikramjit Singh
; APPLICANT: Kalichman, Michael
; TITLE OF INVENTION: Apoptosis Modulators That Interact with the
; TITLE OF INVENTION: Huntington's Disease Gene

NUMBER OF SEQUENCES: 44
CORRESPONDENCE ADDRESS:
ADDRESSEE: Opedahl & Larson
STREET: PO Box 5270
CITY: Ftisco
STATE: CO
COUNTRY: USA
ZIP: 80443-5270
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.44 Kb storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS DOS 5.0
SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/085,199B
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Larson, Marina T.
REGISTRATION NUMBER: 32038
REFERENCE/DOCKET NUMBER: UBC.P-0130S2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (970) 668-2050
TELEFAX: (970) 668-2052
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 4796
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: no
ANTI-SENSE: no
ORIGINAL SOURCE:
ORGANISM: human
FEATURE:
OTHER INFORMATION: cDNA for Huntington-interacting protein
US-09-085-199B-3
Query Match 39.7%; Score 23.8; DB 4; Length 4796;
Best Local Similarity 66.7%; Pred. No. 7.8; Mismatches 17; Indels 0; Gaps 0;
Matches 34; Conservative 0; Mismatches 17; Indels 0; Gaps 0;
QY 10 ACTCTGCGCAATATTTGAAGACGTAAGACGACGACGACACACATGAAAGAA 60
DB 3539 AGTTGTGCAATGATGAAACTGAAAGACTGAGAGAAAGAAAGAAAGAA 3489
RESULT 4
US-09-472-971-5
; Sequence 5, Application US/09472971
; Patent No. 6197547
; GENERAL INFORMATION:
; APPLICANT: Sogo, Kazuo
; APPLICANT: Yanagi, Hideki
; APPLICANT: Yura, Takashi
; TITLE OF INVENTION: TRIGGER FACTOR EXPRESSION PLASMIDS
; FILE REFERENCE: 1423-409P
; CURRENT APPLICATION NUMBER: US/09/472,971
; CURRENT FILING DATE: 1999-12-28
; EARLIER APPLICATION NUMBER: JP10-372965
; EARLIER FILING DATE: 1998-12-28
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 5
; LENGTH: 1647
; TYPE: DNA
; ORGANISM: Escherichia coli
; US-09-472-971-5
Query Match 39.3%; Score 23.6; DB 4; Length 1647;
Best Local Similarity 69.6%; Pred. No. 7.1; Mismatches 14; Indels 0; Gaps 0;
Matches 32; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

OY	12	TCTGTGCGAATATTGAAGACGTTAAGCACTGCAGCACAACATGAAAA	57
Db	1046	TCCGTACAGCATTTGAAGAAGCAACTTCTGACTACGACCGTGAAAA	1091

RESULT 5
US-09-472-971-7
; Sequence 7, Application US/09472971
; Patent No. 6107547

```

? ORGANISM: Escherichia coli
?
? US-09-472-971-7
?
? CURRENT INVENTION:
? APPLICANT: SOGO, Kazuyo
? APPLICANT: YANAGI, Hideki
? APPLICANT: YURA, Takashi
? TITLE OF INVENTION: TRIGGER FACTOR EXPRESSION PLASMIDS
? FILE REFERENCE: 1422-409P
? CURRENT APPLICATION NUMBER: US/09/472,971
? CURRENT FILING DATE: 1999-12-28
? EARLIER APPLICATION NUMBER: JP10-372965
? EARLIER FILING DATE: 1998-12-28
? NUMBER OF SEQ ID NOS: 7
? SOFTWARE: PatentIn Ver. 2.1
?
? SEQ ID NO 7
? LENGTH: 4524
? TYPE: DNA
?
? ORGANISM: Escherichia coli
?
? US-09-472-971-7

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Query Match          39.3%; Score 23.6; DB 4; Length 4524;
Best Local Similarity 69.6%; Pred. No. 9.1;
Matches 32; Conservative 0; Mismatches 14; Indels 0;

QY      12 TCTGTGCAATATTTGAAGACGTAAGACTGACGACAACATGAANA 57
         || || | || || || || || || || || || || || || ||
Db      1428 TCCGTACAGACAGATTGAAGAGACCACTTCTGACTACGACCGTGAANA 1473

RESULT 6
US-09-404-879A-27/c
; Sequence 27, Application US/09404879A
; Patent No. 6468346

```

```

: APPLICANT: Mitchell, Jennifer L.
: APPLICANT: Kling, Gordon E.
: APPLICANT: Algate, Paul A.
: TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
: TITLE OF INVENTION: DIAGNOSIS OF OVARIAN CANCER
: FILE REFERENCE: 210121.462C2
: CURRENT APPLICATION NUMBER: US/09/404,879A
: CURRENT FILING DATE: 1999-09-24
: NUMBER OF SEQ ID NOS: 393
: SOFTWARE: FastSeq for Windows Version 3.0
: SEQ ID NO 27
: LENGTH: 461
: TYPE: DNA
: ORGANISM: Homo sapien
: FEATURE:
: NAME/KEY: misc_feature
: LOCATION: (1)...(461)
: OTHER INFORMATION: n = A,T,C or G
: US-09-404-879A-27

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RESULT 7
US-09-404-879A-74

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Sequence 74, Application US/090404879A
Patient No. 6468546
GENERAL INFORMATION:
APPLICANT: Mitcham, Jennifer L.
APPLICANT: King, Gordon E.
APPLICANT: Algate, Paul A.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF OVARIAN CANCER
FILE REFERENCE: 210121.462022
CURRENT APPLICATION NUMBER: US/09/404,879A
CURRENT FILING DATE: 1999-09-24
NUMBER OF SEQ ID NOS: 393
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 74
LENGTH: 1567
TYPE: DNA
ORGANISM: Homo sapien
US-09-404-879A-74

```

Query Match	38.7%;	Score 23.2;	DB 4;	Length 1567;
Best Local Similarity	61.7%;	Pred. No. 9.8;		
Matches 37; Conservative	0;	Mismatches 23;	Indels 0;	Gaps 0;

```

RESULTS 8
US-09-404-879A-391
: Sequence 391, Application US/09404879A
: Patent No. 6468546
: GENERAL INFORMATION:
: APPLICANT: Mitcham, Jennifer L.
: APPLICANT: King, Gordon E.
: TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
: TITLE OF INVENTION: DIAGNOSIS OF OVARIAN CANCER
: FILE REFERENCE: 210121.462C2
: CURRENT APPLICATION NUMBER: US/09/404,879A
: CURRENT FILING DATE: 1999-09-24
: NUMBER OF SEQ ID NOS: 393
: SOFTWARE: FastSeq for Windows Version 3.0
: SEQ ID NO 391
: LENGTH: 2627
: TYPE: DNA
: ORGANISM: Homo sapiens
US-09-404-879A-391

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Query Match	38.7%	Score 23.2;	DB 4;	Length 2627;
Best Local Similarity	61.7%	Pred. No. 11;		
Matches 37; Conservative	0;	Mismatches 23;	Indels 0;	Gaps 0;

RESULT 9
 US-08-358-160-139/c
 ; Sequence 139, Application US/08358160
 ; Patent No. 5663143
 ;
 ; GENERAL INFORMATION:
 ;
 ; APPLICANT: LEY, Arthur C.
 ; APPLICANT: LADNER, Robert C.
 ; APPLICANT: GUTERMAN, Sonia K.
 ; APPLICANT: ROBERTS, Bruce L.
 ; APPLICANT: MARKLAND, William
 ; APPLICANT: KENT, Rachel B.
 ;
 ; TITLE OF INVENTION: ENGINEERED HUMAN-DERIVED KUNITZ
 ; TITLE OF INVENTION: DOMAINS THAT INHIBIT HUMAN NEUTROPHIL ELASTASE
 ;
 ; NUMBER OF SEQUENCES: 234
 ;
 ; CORRESPONDENCE ADDRESS:

ADDRESSEE: BROWDY AND NEIMARK
STREET: 419 Seventh Street, N.W. Suite 300
CITY: Washington
STATE: District of Columbia
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/358,160
FILING DATE: 16-DEC-1994
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/133,031
FILING DATE: 13-OCT-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/009,319
FILING DATE: 26-JAN-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/664,989
FILING DATE: 01-MAR-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/487,063
FILING DATE: 02-MAR-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/240,160
FILING DATE: 02-SEP-1988
ATTORNEY/AGENT INFORMATION:
NAME: Cooper, Iver P.
REGISTRATION NUMBER: 28,005
REFERENCE/DOCKET NUMBER: LEY-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
TELEX: 248633
INFORMATION FOR SEQ ID NO: 139:
SEQUENCE CHARACTERISTICS:
LENGTH: 189 bases
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: synthetic DNA fragment
US-08-358-160-139

Query Match 37.3%; Score 22.4; DB 1; Length 189;
Best Local Similarity 60.0%; Pred. No. 11;
Matches 27; Conservative 4; Mismatches 14; Indels 0; Gaps 0;

QY 15 GTGCGAATATTGAAGACGTAGCAGCAGCAACATGAAGA 59
DB 89 GTGAATGTGAAGAAASHAAGCSNKGAGANASCAAYACANAGA 45

RESULT 10
US-09-138-024-20/c
Sequence 20, Application US/09138024A
Patent No. 6004779
GENERAL INFORMATION:
APPLICANT: Bradley, John D.
APPLICANT: Thompson, Craig M.
APPLICANT: Moore, Jeffrey B.
APPLICANT: Mobbe, C. Richard
APPLICANT: Healy, Judith M.
APPLICANT: Donnelly, Caroline E.
TITLE OF INVENTION: REGULATED GENE EXPRESSION IN YEAST
FILE REFERENCE: 0342/1D4690S1
CURRENT APPLICATION NUMBER: US/09/138,024A
CURRENT FILING DATE: 1998-08-21
EARLIER APPLICATION NUMBER: 60/056,719

EARLIER FILING DATE: 1997-08-22
NUMBER OF SEQ ID NOS: 24
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 20
LENGTH: 7102
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Plasmid pzm195
US-09-138-024-20

Query Match 37.3%; Score 22.4; DB 3; Length 7102;
Best Local Similarity 66.7%; Pred. No. 28;
Matches 32; Conservative 0; Mismatches 16; Indels 0; Gaps 0;

QY 10 ACTCTGCGAATATTGAAGACGTAGCAGCAGCAACATGAAGA 57
DB 476 ATTATATCGAAATTTATAAAGAAAGCATGAGAAACATTAAAA 429

RESULT 11
US-09-404-066-20/c
Sequence 20, Application US/09404066
Patent No. 6365409
GENERAL INFORMATION:
APPLICANT: Bradley, John D.
APPLICANT: Thompson, Craig M.
APPLICANT: Moore, Jeffrey B.
APPLICANT: Mobbe, C. Richard
APPLICANT: Healy, Judith M.
APPLICANT: Donnelly, Caroline E.
TITLE OF INVENTION: REGULATED GENE EXPRESSION IN YEAST
FILE REFERENCE: 0342/1D4690S1
CURRENT APPLICATION NUMBER: US/09/404,066
CURRENT FILING DATE: 1999-09-23
PRIOR APPLICATION NUMBER: US 09/138,024
PRIOR FILING DATE: 1998-08-21
PRIOR APPLICATION NUMBER: 60/056,719
PRIOR FILING DATE: 1997-08-22
NUMBER OF SEQ ID NOS: 24
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 20
LENGTH: 7102
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Plasmid pzm195
US-09-404-066-20

Query Match 37.3%; Score 22.4; DB 4; Length 7102;
Best Local Similarity 66.7%; Pred. No. 28;
Matches 32; Conservative 0; Mismatches 16; Indels 0; Gaps 0;

QY 10 ACTCTGCGAATATTGAAGACGTAGCAGCAGCAACATGAAGA 57
DB 476 ATTATATCGAAATTTATAAAGAAAGCATGAGAAACATTAAAA 429

RESULT 12
US-08-967-101-5/c
Sequence 5, Application US/08967101
Patent No. 5840540
GENERAL INFORMATION:
APPLICANT: ST. GEORGE-HYSLOP, PETER H
APPLICANT: ROMMENS, JOHANNA M
APPLICANT: FRASER, PAUL E
TITLE OF INVENTION: GENETIC SEQUENCES AND PROTEINS RELATED
TITLE OF INVENTION: TO ALZHEIMER'S DISEASE
NUMBER OF SEQUENCES: 183
CORRESPONDENCE ADDRESS:
ADDRESSEE: TESTA, HURWITZ & THIBEAULT
STREET: High Street Tower - 125 High Street
CITY: Boston

STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02110
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/967,101
FILING DATE: 10-NOV-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/592,541
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Pitcher, Edmund R.
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 248-7000
TELEFAX: (617) 248-7100
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 3087 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
US-08-967-101-5

Query Match 37.0%; Score 22.2; DB 2; Length 3087;
Best Local Similarity 63.5%; Pred. No. 27;
Matches 33; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

QY 9 CACTCTGCGCAATTTGAGACGTAAGCACTGAGACACATGAAAGAA 60
DB 375 CACTATGATTATANTGCTTAAGCAGAGCTGACCACACGCGTGAAGAA 324

RESULT 13

US-08-592-541-5/c
Sequence 5, Application US/08592541
Patent No. 5986054

GENERAL INFORMATION:
APPLICANT: ST. GEORGE-HYSLOP, PETER H
APPLICANT: ROMMENS, JOHANNA M
ATTORNEY/AGENT INFORMATION:
NAME: Pitcher, Edmund R.
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 248-7000
TELEFAX: (617) 248-7100
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 3087 base pairs

TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
US-08-592-541-5

Query Match 37.0%; Score 22.2; DB 2; Length 3087;
Best Local Similarity 63.5%; Pred. No. 27;
Matches 33; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

QY 9 CACTCTGCGCAATTTGAGACGTAAGCACTGAGACACATGAAAGAA 60
DB 375 CACTATGATTATANTGCTTAAGCAGAGCTGACCACACGCGTGAAGAA 324

RESULT 14

US-09-124-698-5/c
Sequence 5, Application US/09124698
Patent No. 6117978

GENERAL INFORMATION:
APPLICANT: ST. GEORGE-HYSLOP, PETER H
APPLICANT: ROMMENS, JOHANNA M
ATTORNEY/AGENT INFORMATION:
NAME: Pitcher, Edmund R.
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 248-7000
TELEFAX: (617) 248-7100
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 3087 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
US-09-124-698-5

Query Match 37.0%; Score 22.2; DB 3; Length 3087;
Best Local Similarity 63.5%; Pred. No. 27;
Matches 33; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

QY 9 CACTCTGCGCAATTTGAGACGTAAGCACTGAGACACATGAAAGAA 60
DB 375 CACTATGATTATANTGCTTAAGCAGAGCTGACCACACGCGTGAAGAA 324

GENERAL INFORMATION:
APPLICANT: ST. GEORGE-HYSLOP, PETER H
APPLICANT: ROMMENS, JOHANNA M
ATTORNEY/AGENT INFORMATION:
NAME: Pitcher, Edmund R.
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 248-7000
TELEFAX: (617) 248-7100
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 3087 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
US-09-124-698-5

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: APPLICANT: ST. GEORGE-HISLOP, PETER H
: APPLICANT: ROMMENS, JOHANNA M
: APPLICANT: FRASER, PAUL E
: TITLE OF INVENTION: GENETIC SEQUENCES AND PROTEINS RELATED
: TITLE OF INVENTION: TO ALZHEIMER'S DISEASE
: NUMBER OF SEQUENCES: 183
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: TESTA, HURWITZ & THIBEAULT
: STREET: High Street Tower - 125 High Street
: CITY: Boston
: STATE: Massachusetts
: COUNTRY: U.S.A.
: ZIP: 02110
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/09/127,480
: FILING DATE:
: CLASSIFICATION:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US/08/592,541
: FILING DATE:
: ATTORNEY/AGENT INFORMATION:
: NAME: Pitcher, Edmund R.
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (617) 248-7000
: TELEFAX: (617) 248-7100
: INFORMATION FOR SEQ ID NO: 5:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 3087 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: cDNA
: US-09-127-480-5

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Query Match          37.0%; Score 22.2; DB 4; Length 3087;
Best Local Similarity 63.5%; Pred. No. 27;
Matches 33; Conservative 0; Mismatches 19; Indels 0; Gaps 0;
QY 9 CACCTGTGCGAATATGAGACGTAGCACTGACGACACATGAAAGAA 60
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DB 375 CACTATGATTAAATGCTTAAGACAGAGCTGACCAACGCTGAGAGAA 324

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Search completed: May 24, 2003, 15:37:35
 Job time : 27.8387 secs

GenCore version 5.1.4.P5.4578
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OM nucleic - nucleic search, using sw model

Run on: May 24, 2003, 13:48:31 ; Search time:46.7742 seconds
(without alignments)
1693.834 Million cell updates/sec

Title: US-09-963-803-9

Perfect score: 60

Sequence: 1 agccatgacactctgtgcga.....gacgacaacatgaagaaga 60

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IDENTITY_NUC
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Searched: 828747 seqs, 660231138 residues

Total number of hits satisfying chosen parameters: 1657494

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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13: /cgn2_6/ptodata/2/pubpna/US60_NEM_PUB.seq:*
14: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match Length	ID	Description
1	60	100.0	60 9 US-09-963-803-9	Sequence 9, Appl1
2	60	100.0	317 9 US-09-963-803-3	Sequence 3, Appl1
3	60	100.0	348 9 US-09-963-803-4	Sequence 4, Appl1
4	60	100.0	392 9 US-09-963-803-21	Sequence 21, Appl1
5	60	100.0	393 9 US-09-963-803-19	Sequence 19, Appl1
6	60	100.0	462 9 US-09-963-803-20	Sequence 20, Appl1
7	60	100.0	600 9 US-09-963-803-22	Sequence 22, Appl1
8	55.4	92.3	301 9 US-09-963-803-7	Sequence 7, Appl1
9	55.4	92.3	371 9 US-09-963-803-5	Sequence 5, Appl1
10	55.4	92.3	398 9 US-09-963-803-6	Sequence 6, Appl1
11	55.4	92.3	472 9 US-09-963-803-25	Sequence 25, Appl1
12	55.4	92.3	541 9 US-09-963-803-24	Sequence 24, Appl1
13	55.4	92.3	604 9 US-09-963-803-23	Sequence 23, Appl1
14	40.4	67.3	515 9 US-09-963-803-2	Sequence 2, Appl1
15	40.4	67.3	532 9 US-09-765-555-1	Sequence 1, Appl1
16	40.4	67.3	8340 10 US-09-847-057-4	Sequence 4, Appl1
17	40.4	67.3	8340 10 US-09-874-926-4	Sequence 4, Appl1
18	40.4	67.3	12241 12 US-10-033-190-5	Sequence 5, Appl1
19	24.6	41.0	1488 9 US-09-891-641-25	Sequence 25, Appl1

c	20	24.4	40.7	513509	9	US-09-754-853A-4	Sequence 4, Appl1
	21	24.2	40.3	2259	10	US-09-815-242-9323	Sequence 9323, Ap
	22	24.2	40.3	2259	10	US-09-815-242-9563	Sequence 9563, Ap
	23	23.8	38.7	272	10	US-09-850-178-31	Sequence 31, Appl
c	24	23.8	39.7	518	10	US-09-864-761-13307	Sequence 13307, A
	25	23.6	39.3	367	10	US-09-764-877-65	Sequence 65, Appl
	26	23.6	39.3	373	7	US-08-781-986A-1139	Sequence 1139, Ap
	27	23.6	39.3	400	7	US-08-781-986A-3782	Sequence 3782, Ap
	28	23.6	39.3	2155	10	US-09-960-428-13	Sequence 13, Appl
	29	23.6	39.3	4473	10	US-09-815-242-4513	Sequence 4513, Ap
	30	23.6	39.3	4509	10	US-09-815-242-8064	Sequence 8064, Ap
c	31	23.6	39.3	30246	7	US-08-781-986A-56	Sequence 56, Appl
c	32	23.4	39.0	802	10	US-09-867-550-1365	Sequence 1365, Ap
c	33	23.2	38.7	281	10	US-09-850-178-4	Sequence 4, Appl1
	34	23.2	38.7	285	9	US-10-015-219-1338	Sequence 1338, Ap
	35	23.2	38.7	285	10	US-09-777-564-1338	Sequence 1338, Ap
	36	23.2	38.7	352	10	US-09-867-701-6377	Sequence 6377, Ap
c	37	23.2	38.7	391	10	US-09-867-701-3918	Sequence 3918, Ap
c	38	23.2	38.7	422	10	US-09-867-701-4906	Sequence 4906, Ap
c	39	23.2	38.7	426	10	US-09-867-701-4161	Sequence 4161, Ap
c	40	23.2	38.7	442	10	US-09-867-701-2832	Sequence 2832, Ap
c	41	23.2	38.7	461	9	US-09-907-969-27	Sequence 27, Appl
c	42	23.2	38.7	461	10	US-09-884-441-27	Sequence 27, Appl
c	43	23.2	38.7	486	10	US-09-867-701-1482	Sequence 1482, Ap
c	44	23.2	38.7	524	10	US-09-867-701-2301	Sequence 2301, Ap
	45	23.2	38.7	555	10	US-09-833-790-388	Sequence 388, App

ALIGNMENTS

RESULT 1
US-09-963-803-9
Sequence 9, Application US/09963803
Publication No. US20030028922A1
GENERAL INFORMATION:
APPLICANT: Meristem Therapeutics
TITLE OF INVENTION: Chimeric expression promoters originating from commelina yello
FILE REFERENCE: 184332042
CURRENT APPLICATION NUMBER: US/09/963,803
CURRENT FILING DATE: 2001-09-26
PRIOR APPLICATION NUMBER: FR 99/03925
PRIOR FILING DATE: 1999-03-29
PRIOR APPLICATION NUMBER: PCT IB00/00370
PRIOR FILING DATE: 2000-10-05
NUMBER OF SEQ ID NOS: 39
SOFTWARE: PatentIn version 3.1
SEQ ID NO 9
LENGTH: 60
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Directional desoxynucleotide building block
US-09-963-803-9
Query Match
Best Local Similarity 100.0%; Score 60; DB 9; Length 60;
Matches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 AGCCATGACACTCTGTGCGAATATTGACAGCGTAACGACGACGACACATGAAAGAA 60
DB 1 AGCCATGACACTCTGTGCGAATATTGACAGCGTAACGACGACGACGACACATGAAAGAA 60
RESULT 2
US-09-963-803-3
Sequence 3, Application US/09963803
Publication No. US20030028922A1
GENERAL INFORMATION:
APPLICANT: Meristem Therapeutics
TITLE OF INVENTION: Chimeric expression promoters originating from commelina yello

;; TITLE OF INVENTION: virus and cassava vein mosaic virus
;; FILE REFERENCE: 184332042
;; CURRENT APPLICATION NUMBER: US/09/963,803
;; CURRENT FILING DATE: 2001-09-26
;; PRIOR APPLICATION NUMBER: FR 99/03925
;; PRIOR FILING DATE: 1999-03-29
;; PRIOR APPLICATION NUMBER: PCT IB00/00370
;; PRIOR FILING DATE: 2000-10-05
;; NUMBER OF SEQ ID NOS: 39
;; SOFTWARE: PatentIn version 3.1
;; SEQ ID NO 3
;; LENGTH: 317
;; TYPE: DNA
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: Promoter MP1116
;; NAME/KEY: promoter
;; LOCATION: (1)..(317)
;; OTHER INFORMATION:
US-09-963-803-3

Query Match 100.0%; Score 60; DB 9; Length 317;
Best Local Similarity 100.0%; Pred. No. 1.2e-12;
Matches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 AGCCATGACACTCTGTGGCAATATTGAAGACGTAAAGCACTGACGACACCAATGAAAGAA 60
Db 73 AGCCATGACACTCTGTGGCAATATTGAAGACGTAAAGCACTGACGACACCAATGAAAGAA 132

RESULT 3
US-09-963-803-4
;; Sequence 4, Application US/09963803
;; Publication No. US20030028922A1
;; GENERAL INFORMATION:
;; APPLICANT: Meristem Therapeutics
;; TITLE OF INVENTION: Chimeric expression promoters originating from commelina yellow
;; FILE REFERENCE: 184332042
;; CURRENT APPLICATION NUMBER: US/09/963,803
;; CURRENT FILING DATE: 2001-09-26
;; PRIOR APPLICATION NUMBER: FR 99/03925
;; PRIOR FILING DATE: 1999-03-29
;; PRIOR APPLICATION NUMBER: PCT IB00/00370
;; PRIOR FILING DATE: 2000-10-05
;; NUMBER OF SEQ ID NOS: 39
;; SOFTWARE: PatentIn version 3.1
;; SEQ ID NO 4
;; LENGTH: 348
;; TYPE: DNA
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: Promoter MP1117
;; NAME/KEY: promoter
;; LOCATION: (1)..(348)
;; OTHER INFORMATION:
US-09-963-803-4

Query Match 100.0%; Score 60; DB 9; Length 348;
Best Local Similarity 100.0%; Pred. No. 1.2e-12;
Matches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 AGCCATGACACTCTGTGGCAATATTGAAGACGTAAAGCACTGACGACACCAATGAAAGAA 60
Db 107 AGCCATGACACTCTGTGGCAATATTGAAGACGTAAAGCACTGACGACACCAATGAAAGAA 166

RESULT 4
US-09-963-803-21
;; Sequence 21, Application US/09963803
;; Publication No. US20030028922A1

;; GENERAL INFORMATION:
;; APPLICANT: Meristem Therapeutics
;; TITLE OF INVENTION: Chimeric expression promoters originating from commelina yellow
;; FILE REFERENCE: 184332042
;; CURRENT APPLICATION NUMBER: US/09/963,803
;; CURRENT FILING DATE: 2001-09-26
;; PRIOR APPLICATION NUMBER: FR 99/03925
;; PRIOR FILING DATE: 1999-03-29
;; PRIOR APPLICATION NUMBER: PCT IB00/00370
;; PRIOR FILING DATE: 2000-10-05
;; NUMBER OF SEQ ID NOS: 39
;; SOFTWARE: PatentIn version 3.1
;; SEQ ID NO 21
;; LENGTH: 392
;; TYPE: DNA
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: Promoter MP1164
;; NAME/KEY: promoter
;; LOCATION: (1)..(392)
;; OTHER INFORMATION:
US-09-963-803-21

Query Match 100.0%; Score 60; DB 9; Length 392;
Best Local Similarity 100.0%; Pred. No. 1.3e-12;
Matches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 AGCCATGACACTCTGTGGCAATATTGAAGACGTAAAGCACTGACGACACCAATGAAAGAA 60
Db 75 AGCCATGACACTCTGTGGCAATATTGAAGACGTAAAGCACTGACGACACCAATGAAAGAA 134

RESULT 5
US-09-963-803-19
;; Sequence 19, Application US/09963803
;; Publication No. US20030028922A1
;; GENERAL INFORMATION:
;; APPLICANT: Meristem Therapeutics
;; TITLE OF INVENTION: Chimeric expression promoters originating from commelina yellow
;; FILE REFERENCE: 184332042
;; CURRENT APPLICATION NUMBER: US/09/963,803
;; CURRENT FILING DATE: 2001-09-26
;; PRIOR APPLICATION NUMBER: FR 99/03925
;; PRIOR FILING DATE: 1999-03-29
;; PRIOR APPLICATION NUMBER: PCT IB00/00370
;; PRIOR FILING DATE: 2000-10-05
;; NUMBER OF SEQ ID NOS: 39
;; SOFTWARE: PatentIn version 3.1
;; SEQ ID NO 19
;; LENGTH: 393
;; TYPE: DNA
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: Promoter MP1162
;; NAME/KEY: promoter
;; LOCATION: (1)..(393)
;; OTHER INFORMATION:
US-09-963-803-19

Query Match 100.0%; Score 60; DB 9; Length 393;
Best Local Similarity 100.0%; Pred. No. 1.3e-12;
Matches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 AGCCATGACACTCTGTGGCAATATTGAAGACGTAAAGCACTGACGACACCAATGAAAGAA 60
Db 75 AGCCATGACACTCTGTGGCAATATTGAAGACGTAAAGCACTGACGACACCAATGAAAGAA 134

RESULT 6

US-09-963-803-20
; Sequence 20, Application US/09963803
; Publication No. US20030028922A1
; GENERAL INFORMATION:
; APPLICANT: Meristem Therapeutics
; TITLE OF INVENTION: Chimeric expression promoters originating from commelina yellow m
; TITLE OF INVENTION: Virus and cassava vein mosaic virus
; FILE REFERENCE: 184332042
; CURRENT APPLICATION NUMBER: US/09/963,803
; PRIOR FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: FR 99/03925
; PRIOR FILING DATE: 1999-03-29
; PRIOR APPLICATION NUMBER: PCT IB00/00370
; PRIOR FILING DATE: 2000-10-05
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 20
; LENGTH: 462
; TYPE: DNA
; ORGANISM: Artificial Sequence
; OTHER INFORMATION: promoter MP1163
; FEATURE:
; NAME/KEY: promoter
; LOCATION: (1)..(462)
; OTHER INFORMATION:
US-09-963-803-20

Query Match 100.0%; Score 60; DB 9; Length 462;
Best Local Similarity 100.0%; Pred. No. 1,3e-12;
Matches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ACCCATGACACTCTGTGCGAATATTGAGACGTAAGCACTGACGACACAAATGAAAAGAA 60
DB 75 ACCCATGACACTCTGTGCGAATATTGAGACGTAAGCACTGACGACACAAATGAAAAGAA 134

RESULT 7

US-09-963-803-22
; Sequence 22, Application US/09963803
; Publication No. US20030028922A1
; GENERAL INFORMATION:
; APPLICANT: Meristem Therapeutics
; TITLE OF INVENTION: Chimeric expression promoters originating from commelina yellow m
; TITLE OF INVENTION: Virus and cassava vein mosaic virus
; FILE REFERENCE: 184332042
; CURRENT APPLICATION NUMBER: US/09/963,803
; PRIOR FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: FR 99/03925
; PRIOR FILING DATE: 1999-03-29
; PRIOR APPLICATION NUMBER: PCT IB00/00370
; PRIOR FILING DATE: 2000-10-05
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 22
; LENGTH: 600
; TYPE: DNA
; ORGANISM: Artificial Sequence
; OTHER INFORMATION: promoter MP1165
; FEATURE:
; NAME/KEY: promoter
; LOCATION: (1)..(600)
; OTHER INFORMATION:
US-09-963-803-22

Query Match 100.0%; Score 60; DB 9; Length 600;
Best Local Similarity 100.0%; Pred. No. 1,4e-12;
Matches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ACCCATGACACTCTGTGCGAATATTGAGACGTAAGCACTGACGACACAAATGAAAAGAA 60
DB 75 ACCCATGACACTCTGTGCGAATATTGAGACGTAAGCACTGACGACACAAATGAAAAGAA 134

RESULT 8
US-09-963-803-7
; Sequence 7, Application US/09963803
; Publication No. US20030028922A1
; GENERAL INFORMATION:
; APPLICANT: Meristem Therapeutics
; TITLE OF INVENTION: Chimeric expression promoters originating from commelina yellow
; TITLE OF INVENTION: Virus and cassava vein mosaic virus
; FILE REFERENCE: 184332042
; CURRENT APPLICATION NUMBER: US/09/963,803
; PRIOR FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: FR 99/03925
; PRIOR FILING DATE: 1999-03-29
; PRIOR APPLICATION NUMBER: PCT IB00/00370
; PRIOR FILING DATE: 2000-10-05
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 7
; LENGTH: 301
; TYPE: DNA
; ORGANISM: Artificial Sequence
; OTHER INFORMATION: promoter MP1154
; FEATURE:
; NAME/KEY: promoter
; LOCATION: (1)..(301)
; OTHER INFORMATION:
US-09-963-803-7

Query Match 92.3%; Score 55.4; DB 9; Length 301;
Best Local Similarity 98.2%; Pred. No. 5.7e-11;
Matches 56; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 4 CATGACACTCTGTGCGAATATTGAGACGTAAGCACTGACGACACAAATGAAAAGAA 60
DB 63 CATGACACTCTGTGCGAATATTGAGACGTAAGCACTGACGACACAAATGAAAAGAA 119

RESULT 9
US-09-963-803-5
; Sequence 5, Application US/09963803
; Publication No. US20030028922A1
; GENERAL INFORMATION:
; APPLICANT: Meristem Therapeutics
; TITLE OF INVENTION: Chimeric expression promoters originating from commelina yellow
; TITLE OF INVENTION: Virus and cassava vein mosaic virus
; FILE REFERENCE: 184332042
; CURRENT APPLICATION NUMBER: US/09/963,803
; PRIOR FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: FR 99/03925
; PRIOR FILING DATE: 1999-03-29
; PRIOR APPLICATION NUMBER: PCT IB00/00370
; PRIOR FILING DATE: 2000-10-05
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 371
; TYPE: DNA
; ORGANISM: Artificial Sequence
; OTHER INFORMATION: promoter MP1146
; FEATURE:
; NAME/KEY: promoter
; LOCATION: (1)..(371)
; OTHER INFORMATION:
US-09-963-803-5

Query Match 92.3%; Score 55.4; DB 9; Length 371;
Best Local Similarity 98.2%; Pred. No. 6e-11;
Matches 56; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

US-09-963-803-23

Query Match 92.3%; Score 55.4; DB 9; Length 604;
Best Local Similarity 98.2%; Pred. No. 6.9e-11;
Matches 56; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 CATGACACTCTGTGGCAATATGAGACGTAGACACTGACGACACATGAAAGAA 60
|||||
DB 160 CATGCCACTCTGTGGCAATATGAGACGTAGACACTGACGACACATGAAAGAA 216

RESULT 14
US-09-963-803-2
; Sequence 2, Application US/09963803
; Publication No. US20030028922A1
; GENERAL INFORMATION:
; APPLICANT: Meristem Therapeutics
; TITLE OF INVENTION: Chimeric expression promoters originating from commelina yellow m
; FILE REFERENCE: 184332042
; CURRENT APPLICATION NUMBER: US/09/963,803
; PRIOR FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: FR 99/03925
; PRIOR FILING DATE: 1999-03-29
; PRIOR APPLICATION NUMBER: PCT IB00/00370
; PRIOR FILING DATE: 2000-10-05
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 515
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Promoter from the intergenic region of Cassava Vein Mosaic virus.
; OTHER INFORMATION: of 515 bp in length EMBL
; NAME/KEY: Promoter
; LOCATION: (1)..(515)
; OTHER INFORMATION:
US-09-963-803-2

Query Match 67.3%; Score 40.4; DB 9; Length 515;
Best Local Similarity 97.6%; Pred. No. 2.1e-05;
Matches 41; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 19 GAATTTGAAGACGTAGACACTGACGACACATGAAAGAA 60
|||||
DB 216 GAATCTTGAAGACGTAGACACTGACGACACATGAAAGAA 257

RESULT 15
US-09-765-555-1
; Sequence 1, Application US/09765555
; Publication No. US20030037355A1
; GENERAL INFORMATION:
; APPLICANT: The Scripps Research Institute
; TITLE OF INVENTION: Methods and compositions to modulate
; FILE REFERENCE: 27801-20014.40
; CURRENT APPLICATION NUMBER: US/09/765,555
; PRIOR FILING DATE: 2002-05-24
; PRIOR APPLICATION NUMBER: US 09/620,897
; PRIOR FILING DATE: 2000-01-21
; PRIOR APPLICATION NUMBER: US 60/177,468
; NUMBER OF SEQ ID NOS: 75
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 532
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Promoter CsmVW

US-09-765-555-1

Query Match 67.3%; Score 40.4; DB 9; Length 532;
Best Local Similarity 97.6%; Pred. No. 2.1e-05;
Matches 41; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 19 GAATTTGAAGACGTAGACACTGACGACACATGAAAGAA 60
|||||
DB 231 GAATCTTGAAGACGTAGACACTGACGACACATGAAAGAA 272

Search completed: May 24, 2003, 15:35:59
Job time : 47.7742 secs

GenCore version 5.1.4.p5.4578
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OM nucleic - nucleic search, using sw model

Run on: May 24, 2003, 11:30:46 / Search time 788.387 Seconds
(Without alignments)
1232.553 Million cell updates/sec

Title: US-09-963-803-9
Perfect score: 60
Sequence: 1 agcagcagcactctgtcga.....gacgacacaaatgaagaagaa 60

Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 16154066 segs, 8097743376 residues
Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

EST:*
1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estnu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_hic:*
9: gb_est1:*
10: gb_est2:*
11: gb_hic:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: gb_gss:*
18: em_gss_hum:*
19: em_gss_inv:*
20: em_gss_pln:*
21: em_gss_vit:*
22: em_gss_fun:*
23: em_gss_mam:*
24: em_gss_mus:*
25: em_gss_other:*
26: em_gss_pro:*
27: em_gss_rnd:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	29.4	49.0	385	9	AU230643 AU230643
C 2	27.2	45.3	424	17	AZ924724 4906.1d55
C 3	27	45.0	667	17	BH108966 RPCI-24-3
C 4	26.4	44.0	431	17	AZ389667 IM0150L03
C 5	26.4	44.0	575	17	AQ633949 RPCI-11-4
C 6	26.2	43.7	192	10	AM605446 PM4-DT006

Result No.	Score	Query Match	Length	ID	Description
C 7	26.2	43.7	658	17	AZ63393 IM0108G23
C 8	25.8	43.0	540	10	AM215182 up05e09.Y
C 9	25.8	43.0	598	10	AV702705
C 10	25.8	43.0	1085	17	CNS0550K
C 11	25.6	42.7	456	13	BM278807
C 12	25.6	42.7	842	12	BF681368
C 13	25.6	42.7	930	12	BG343357
C 14	25.4	42.3	284	13	B118726
C 15	25.4	42.3	489	13	B1813129
C 16	25.4	42.3	500	13	B1812716
C 17	25.2	42.0	510	17	AZ493220
C 18	25	41.7	326	10	AM836970
C 19	25	41.7	524	13	B1812356
C 20	25	41.7	543	17	DR3B14T
C 21	25	41.7	595	10	BE086841
C 22	25	41.7	595	17	AO500652
C 23	25	41.7	669	17	AO480401
C 24	25	41.7	1529	12	BF302770
C 25	24.8	41.3	414	17	AZ913122
C 26	24.8	41.3	541	17	AO927911
C 27	24.8	41.3	698	17	AZ842321
C 28	24.8	41.3	721	17	AZ305083
C 29	24.6	41.0	205	10	BE158588
C 30	24.6	41.0	291	10	AM232994
C 31	24.6	41.0	379	9	A1548520
C 32	24.6	41.0	419	9	A1976090
C 33	24.6	41.0	433	13	B1288988
C 34	24.6	41.0	538	10	BE096573
C 35	24.6	41.0	538	17	AO693720
C 36	24.6	41.0	563	13	BM421339
C 37	24.6	41.0	605	17	BH768803
C 38	24.6	41.0	627	17	BH768819
C 39	24.6	41.0	627	9	A1411341
C 40	24.6	41.0	634	14	BO198811
C 41	24.6	41.0	639	12	BF358001
C 42	24.6	41.0	643	17	AZ498380
C 43	24.6	41.0	695	14	BO973481
C 44	24.6	41.0	920	17	CNS04N3F
C 45	24.6	41.0	1021	13	BG913244

ALIGNMENTS

RESULT 1
LOCUS AU230643/c
DEFINITION AU230643 RAF19 Arabidopsis thaliana cDNA clone RAF19-72-A12 3', mRNA sequence.
ACCESSION AU230643
VERSION AU230643.1 GI:19799353
KEYWORDS EST.
SOURCE
ORGANISM
Chale cress.
Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE
1 (bases 1 to 385)
Seki, M., Narusaka, M., Ishida, J., Kamiya, A., Satou, M., Nakajima, M., Akiyama, K., Enju, A., Oono, Y., Sakurai, T., Carninci, P., Kawai, J., Itoh, M., Ishii, Y., Arakawa, T., Shibata, K., Shinozaki, K., Hayashizaki, Y., and Shinozaki, K.
Large scale analysis of Arabidopsis full-length cDNA
Unpublished (2002)
CONTACT: Motoaki Seki
Plant Functional Genomics Research Group
RIKEN Genomic Sciences Center
3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan
Tel.: 81-298-36-4359
Fax: 81-298-36-9060
Email: mseki@rkc.riken.go.jp
An Arabidopsis full-length cDNA library was constructed essentially as reported previously (Seki et al., 1998). cDNA cleaved with BamHI

JOURNAL	TITLE	
COMMENT	J.M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A., and Wright, D., Weiss, R. Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts	
	Contact: Robert B. Weiss University of Utah Genome Center University of Utah Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT 84112, USA	
	Tel: 801 585 5606 Fax: 801 585 7177 Email: ddunne@genetics.utah.edu	
	Insert Length: 10000 Std Error: 0.00 Plate: 0150 row: L column: 03	
	Seq primer: CACACAGAAACACCTATGACC	
	Class: plasmid ends	
	High quality sequence stop: 431.	
FEATURES	location/Qualifiers	
SOURCE	1. 431	
	/organism="Mus musculus"	
	/strain="C57BL/6J"	
	/db_xref="taxon:10090"	
	/clone="UGC1M015L03"	
	/clone_lib="Mouse 10kb plasmid UGC1M library"	
	/sex="Male"	
	/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"	
	/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PWD42 (g114732114[gb AF129072.1]), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."	
BASE COUNT	95 a 81 c 96 g 159 t	
ORIGIN		
	Query Match 44.0%; Score 26.4; DB 17; Length 431; Best Local Similarity 65.0%; Pred. No. 3.36+02; Matches 39; Conservative 0; Mismatches 21; Indels 0; Gaps 0;	
Oy	1 AGCCATGACACTCTGCGAATATGTGAAGAGCTAGCAGTACGACCAATGAAAGAA 60	
Db	67 AACACTAAACTCAGACGAGAAATTGAATGAATGAATGAAGAAACCAATGCAAGAA 8	
RESULT 5		
A0633949	LOCUS A0633949 575 bp DNA Linear GSS 17-JUN-1999	
DEFINITION	RPCI-11-47811.TV RPCI-11 Homo sapiens genomic clone RPCI-11-47811, DNA sequence.	
ACCESSION	A0633949	
VERSION	A0633949.1 GI:5096584	
KEYWORDS	GSS.	
SOURCE	human.	
ORGANISM	Homo sapiens	
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.	
REFERENCE	1 (bases 1 to 575) Zhao, S., Adams, M.D., Nierman, W., Malek, J., de Jong, P. and Venter, J.C.	

```

TITLE      Use of BAC End Sequences from Library RPCI-11 for Sequence-Ready
JOURNAL    Map Building
COMMENT     Unpublished (1997)
            Other-GSSs: RPCI-11-47811.TJ
            Contact: Shaying Zhao, William Nierman, Mark Adams
            Department of Eukaryotic Genomics
            The Institute for Genomic Research
            9712 Medical Center Dr., Rockville, MD 20850
            Tel: 301 838 0200
            Fax: 301 838 0208
            Email: hbe@tigr.org
            Clones are derived from the human BAC library RPCI-11. For BAC
            library availability, please contact Pieter de Jong
            (pieter@edlong.med.buffalo.edu). Clones may be purchased from
            BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or from
            Research Genet cs (inforesgen.com). BAC end search page:
            http://www.tigr.org/tldb/humgen/bac\_end\_search/bac\_end\_search.html.
            Seq primer: T7
            Class: BAC ends.

FEATURES
SOURCE      Location/Qualifiers
            1..575
                /organism="Homo sapiens"
                /db_xref="GDB:7683360"
                /db_xref="taxon:9606"
                /clone="RPCI-11-47811"
                /clone_11b="RPCI-11"
                /sex="Male"
                /cell_type="Lymphocytes"
                /note="Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI;
                RPCI11 Human Male BAC library"
BASE COUNT  192 a 115 c 102 g 166 t
ORIGIN
Query Match      44.0%; Score 26.4; DB 17; Length 575;
Best Local Similarity 69.2%; Pred. No.3.5e+02;
Matches 36; Conservative 0; Mismatches 16; Indels 0; Gaps 0;

OY      9 CACTCTGTGCGAATATTGAGACGTGACGACTGACGACACATGTAAGAAG 60
          1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
Db      89 CTCCTGTGTGAAGTATCGAAGAGCTAAGCACACAGCTTGTAACAAATGAATAGAA 140
          1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1

RESULT 6
LOCUS      AM605446                      192 bp      mRNA      linear      EST 23-MAR-2000
DEFINITION PM4-DT0067-010200-002-b05 DT0067 Homo sapiens cDNA, mRNA sequence.
ACCESSION  AM605446
VERSION     AM605446.1 GI:7310187
KEYWORDS    EST.
SOURCE      human.
ORGANISM    Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE   1 (bases 1 to 192)
AUTHORS    HGP http://www.ludwig.org.br/GRSSTS.
TITLE      The FAPESP/LICR Human Cancer Genome Project
JOURNAL    Unpublished (1999)
COMMENT     Contact: Simpson A.J.G.
            Laboratory of Cancer Genetics
            Ludwig Institute for Cancer Research
            Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
            Brazil
            Tel: +55-11-7704922
            Fax: +55-11-7707001
            Email: astimpson@ludwig.org.br
            This sequence was derived from the FAPESP/LICR Human Cancer Genome
            Project. This entry can be seen in the following URL
            (http://www.ludwig.org.br/scripts/gethtml2.pl?l1-PM4et2-PM4-DT0067-010200-002-b05et3-2000-02-01et4-1)
            Seq primer: puc 18 forward
            High quality sequence stop: 118.
            Location/Qualifiers
            1..192
FEATURES
SOURCE

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/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_1lb="DT0067"
/dev_stage="Adult"
/note="organ: dentis, drash; Vector: puc18; Site_1: SmaI;
Site_2: SmaI; A mini-library was made by cloning products
derived from ORSTES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."

BASE COUNT 50 a 21 c 61 g 56 t 4 others
ORIGIN

Query Match 43.7%; Score 26.2; DB 10; Length 192;
Best Local Similarity 63.8%; Pred. No. 3.4e+02;
Matches 37; Conservative 0; Mismatches 21; Indels 0; Gaps 0;

QY 3 CCATGACACTCTGCGAATTTGAGAGCTAGCACTGACGACACATGAAAGAA 60
DB 90 CTATGAGCTTGTGGGAAATTTGTATATGTCANNCCACCGACACACTGACAGAA 147

RESULT 7
LOCUS A2363393 658 bp DNA linear GSS 02-OCT-2000
DEFINITION 1M0108G23R Mouse 10kb plasmid UGCCIM library Mus musculus genomic
clone UGCCIM0108G23 R, DNA sequence.
ACCESSION A2363393
VERSION A2363393.1 GI:10477093
KEYWORDS GSS.
SOURCE house mouse.
ORGANISM Mus musculus
Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 658)
REFERENCE Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamill, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, F., Reilly,
M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Delfhausen, A.
and Wright, D., Weis, R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
JOURNAL Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: dunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0108 row: G column: 23
Seq primer: CACACAGAAACAGATGACAC
Class: plasmid ends
High quality sequence stop: 658.
FEATURES
Source location/Qualifiers
1..658
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone_1lb="UGCCIM0108G23"
/clone_1lb="Mouse 10kb plasmid UGCCIM library"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, TI-resistant, F-"
/note="Vector: pMDA2nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were

ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pMD2 (g1147321149b/AR129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adapted mouse DNA was annealed to
adapted vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

BASE COUNT 194 a 165 c 103 g 194 t
ORIGIN

Query Match 43.7%; Score 26.2; DB 17; Length 658;
Best Local Similarity 79.5%; Pred. No. 4.1e+02;
Matches 31; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 22 TATTGAAGCTTAAGCACTGACGACACATGAAAGAA 60
DB 1 TAGTGAAGCTTGAAGCACTGACGACACATGAAAGAA 39

RESULT 8
LOCUS AW215182/c 540 bp mRNA linear EST 06-DEC-1999
DEFINITION up05e09.y1 NCI-CGAP_Lu30 Mus musculus cDNA clone IMAGE:2651176 5'
similar to SW:ERP5_HUMAN Q15084 PROBABLE PROTEIN DISULFIDE
ISOMERASE P5 PRECURSOR ;, mRNA sequence.
ACCESSION AW215182
VERSION AW215182.1 GI:6525793
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus
Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 540)
REFERENCE NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
JOURNAL Contact: Robert Strausberg, Ph.D.
Email: cgaps-remail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
www-bio.11nl.gov/dbp/image/image.html
MGI:1031628
Seq primer: -40RP from Glbco
High quality sequence stop: 241.
FEATURES
Source location/Qualifiers
1..540
/organism="Mus musculus"
/strain="C2EHC II"
/db_xref="taxon:10090"
/clone_1lb="IMAGE:2651176"
/clone_1lb="NCI-CGAP_Lu30"
/tissue_type="tumor, metastatic to mammary"
/lab_host="DH10B"
/note="Organ: lung; Vector: PCMV-SPORT6; Site_1: NotI;
Site_2: SalI; transgenic model WNT-1, expression driven by
MMTV-LTR enhancer; Cloned unidirectionally. Primer: Oligo
dr. library constructed by Life Technologies.
Investigator providing samples: Gilbert Smith, NIH"

BASE COUNT 149 a 125 c 142 g 113 t 11 others
ORIGIN

Query Match 43.0%; Score 25.8; DB 10; Length 540;
Best Local Similarity 64.3%; Pred. No. 5.2e+02;

BASE COUNT	240 a	245 c	257 g	180 t	8 others
ORIGIN					

Query Match	42.7%	Score 25.6	DB 12	Length 930
Best Local Similarity	64.2%	Pred. No. 6.6e+02		
Matches 34	Conservative	0	Mismatches 19	Indels 0
				Gaps 0

QY 8 ACACCTCTGTGGCAATATTGAAGACGTAACCACTGACGACACAACATGAAAAA 60
 |||| | ||| | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 527 ACACGCGGTGTGACTNNTTNAAGACAGAAANNATATATAAGAAAAAAAAAGAA 579

RESULT	14
Bll18726	
LOCUS	284 bp mRNA linear EST 26-JUN-2001
DEFINITION	Fungus differentially expressed cDNA libraries of BRH-treated/laser fungus-infected rice leaf tissues Oryza sativa cDNA clone BHN-n7, mRNA sequence.

ACCESSION	BI118726	GI:14571358
VERSION	BI118726.1	
KEYWORDS	EST.	
SOURCE	<i>Oryza sativa</i> .	
ORGANISM	<i>Oryza sativa</i>	

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta
 Spermatophyta; Magnoliophyta; Liliopsida; Poaceae;
 Erihartoideae; Oryzaceae; Oryza.
 1 (bases 1 to 284)

TITLE	Molecular cloning of differentially expressed cDNAs associated with
JOURNAL	systemic acquired resistance in rice
COMMENT	Unpublished (2001)
	Contact: Song, F.M.; Goodman, R.M.

COMMENT

Contact: Song, F.M.; Goodman, R.M.
Department of Plant Pathology
University of Wisconsin-Madison
Rm 689, Russell Laboratories, 1630 Linden Drive, Madison, WI 53706,
USA
Tel: 608 262 9162
Fax: 608 262 8643
Email: fmsong@plantpath.wisc.edu; rgoodman@facstaff.wisc.edu
Benzo[1,4]diazole-inducible
Insert length: 284 std Error: 0.00
Seq primer: M13 Forward and reverse.

FEATURES

Source

1. .284
/organism="Oryza sativa"
/cultivar="Yuanfengzao (a susceptible variety to rice
blast disease)"
/db_xref="taxon:4530"

clone.lib="Differentially expressed cDNA libraries of BTH-treated/blast fungus-infected rice leaf tissues" /tissue.type="Seedling leaves" /dev.stage="Three-week-old rice seedlings pretreated with BTH and/or inoculated with Magnaporthe grisea" /note="Vector: pGEM-T Easy; Rice seedlings were pretreated by foliar spraying with 0.3 mM benzothiadiazole (BTH) and then inoculated with Magnaporthe grisea three days after BTH treatment. Leaf samples were collected twenty-four hour after inoculation and mRNAs were used for construction of the differentially expressed cDNA libraries."

BASE COUNT
ORIGIN

Query Match

42.38; Score 25.4; DB 13; Length 284;

Best Local Similarity 64.48; Pred. No. 6.3e+02;
Matches 38; Conservative 0; Mismatches 21; Indels 0; Gaps 0;

2 GCCATGACACTCTGTGGCAATATTGAAGACGTAAACACTGACGACACACATGAAAAGAA 60
 11 11 111111 111 1 11111 11 11111 1
 Db 125 GCTCTGTACTCTGTCCGAGTGAAGAAAGACGACGACGACGACGACGCTAAAAAGCA 183

RESULT 15
BI813129/
LOCUS

LOCUS	Bt1813129	489 bp	mRNA	linear	EST 01-NOV-2001
DEFINITION	J002C12	Oryza sativa mature leaf	library	induced by	M.grisea Oryza
ACCESSION	Bt1813129	cDNA clone	J002C12	mRNA sequence.	

ACCESSION	BI813129
VERSION	BI813129.1
EDITION	GI:16579034
DATE	

SOURCE
ORGANISM

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
1 (bases 1 to 480)

REFERENCE	AUTHORS	TITLE	JOURNAL	COMMENT
1 (bases 1 to 489)	Dong,H.T., Li,D.B., Zhuang,X.F., Dai,C.G., Sun,L.X., Pei,Y.X., H.F., Jiang,Y.X., Yu,F.C., Gao,Q.R. and Lou,Y.C.	A Gene Expression Screen in <i>Oryza sativa</i>	Unpublished (2001)	Contact: Dong HT

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Fax: 0086-571-86961525
Email: hcdong@jnuem.zju.edu.cn
Seq primer: M13 forward primer.

FEATURES

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/organism="Oryza sativa"
/db_xref="taxon:4530"
/clone="J002C12"
/clone_lib="Oryza sativa mature leaf library induced by

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BASE COUNT	134 a	108 c	131 g	116 t
ORIGIN				

Query Match	42.3%	Score 25.4	DB 13	length 489
Best Local Similarity	64.4%	Pred. No. 6.8e+02		
Matches 38	Conservative 0	Mismatches 21	Indels 0	Gaps 0

OY 2 GCCATGACACTCTGTGGCATATTGAAGACGTAAGCACTGACGCACAACAAATGAAAAA 60
 || || ||||| || | ||||| | ||||| | ||||| |
Db 290 GCTCTGTGACTCTGTCCGATGAAGAAGACGACGACGACGACGACGCTAAAAAGCA 23

Search completed: May 24, 2003, 15:33:20
Job time : 793.387 secs

